GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 8, 2003, 08:26:59 ; Search time 23 Seconds
(without alignments)
674.731 Million cell updates/sec

Title: US-09-991-225-2
Perfect score: 1712
Sequence: 1 MEPNGTPSNNNSRNCTIENF.....KAKTKCVFPVSVWLRKETRV 330

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1712	100.0	346	1	CLT2_HUMAN	Q9ns75 homo sapien
2	1367.5	79.9	345	1	CLT2_PIG	Q95n03 sus scrofa
3	1197	69.9	309	1	CLT2_MOUSE	Q920a1 mus musculu
4	1187	69.3	309	1	CLT2_RAT	Q924t9 rattus norv
5	567.5	33.1	339	1	CLT1_RAT	Q924t8 rattus norv
6	563	32.9	340	1	CLT1_PIG	Q95n02 sus scrofa
7	560	32.7	352	1	CLT1_MOUSE	Q995a4 mus musculu
8	559	32.7	337	1	CLT1_HUMAN	Q9y271 homo sapien
9	479	28.0	367	1	GP17_HUMAN	Q13304 homo sapien
10	470	27.5	362	1	P2YR_MELGA	P49652 meleagris g
11	467	27.3	362	1	P2YR_CHICK	P34996 gallus gall
12	447	26.1	308	1	P2Y5_CHICK	P32250 gallus gall
13	447	26.1	373	1	P2YR_RAT	P49651 rattus norv
14	446	26.1	373	1	P2YR_HUMAN	P47900 homo sapien
15	442	25.8	373	1	P2YR_BOVIN	P48042 bos taurus
16	442	25.8	373	1	P2YR_MOUSE	P49650 mus musculu
17	440	25.7	361	1	EBI2_HUMAN	P32249 homo sapien
18	436	25.5	344	1	P2Y5_HUMAN	P43657 homo sapien
19	434	25.4	377	1	P2Y2_HUMAN	P41231 homo sapien
20	430	25.1	370	1	P2Y9_HUMAN	Q99677 homo sapien
21	421.5	24.6	374	1	P2Y2_RAT	P41232 rattus norv
22	418.5	24.4	373	1	P2Y2_MOUSE	P35383 mus musculu
23	416	24.3	342	1	PAFR_CAVPO	P21556 cavia porce
24	409.5	23.9	342	1	PAFR_HUMAN	P25105 homo sapien
25	407	23.8	537	1	P2Y8_XENLA	P79928 xenopus lae
26	405	23.7	355	1	CKR1_MACMU	P56482 macaca mula
27	404.5	23.6	420	1	PAR1_XENLA	P47749 xenopus lae
28	404	23.6	341	1	PAFR_MOUSE	Q62035 mus musculu
29	400.5	23.4	397	1	PAR2_HUMAN	P55085 homo sapien
30	398	23.2	380	1	APJ_HUMAN	P35414 homo sapien
31	398	23.2	380	1	APJ_MACMU	Q97666 macaca mula
32	397	23.2	341	1	PAFR_RAT	P46002 rattus norv
33	394.5	23.0	355	1	CKR1_HUMAN	P32246 homo sapien
34	391.5	22.9	355	1	CKR1_MOUSE	P51675 mus musculu
35	391	22.8	328	1	P2Y6_RAT	Q63371 rattus norv
36	390	22.8	399	1	PAR2_MOUSE	P55086 mus musculu
37	389	22.7	361	1	P2Y4_RAT	O35811 rattus norv
38	387	22.6	371	1	CML1_RAT	O35786 rattus norv
39	386	22.5	373	1	CML1_HUMAN	Q99788 homo sapien
40	385.5	22.5	361	1	P2Y4_MOUSE	Q91j87 mus musculu
41	385	22.5	328	1	P2Y3_CHICK	Q98907 gallus gall
42	384	22.4	377	1	APJ_MOUSE	Q9wv08 mus musculu
43	383	22.4	397	1	PAR2_RAT	Q63645 rattus norv
44	382	22.3	371	1	CML1_MOUSE	P97468 mus musculu
45	381.5	22.3	328	1	P2Y3_MELGA	O93361 meleagris g

ALIGNMENTS

```
RESULT 1
CLT2_HUMAN
ID   CLT2_HUMAN      STANDARD;      PRT;   346 AA.
AC   Q9NS75; Q9HCQ2;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Cysteinyl leukotriene receptor 2 (CysLTR2) (PSEC0146) (HG57) (HPN321)
DE   (hGPCR21).
GN   CYSLTR2 OR CYSLT2 OR CYSLT2R.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=20374466; PubMed=10913337;
RA   Takasaki J., Kamohara M., Matsumoto M., Saito T., Sugimoto T., Ota T.,
RA   Nishikawa T., Kawai Y., Masuho Y., Isogai T., Suzuki Y., Sugano S.,
RA   Furuichi K.;
RT   "The molecular characterization and tissue distribution of the human
RT   cysteinyl leukotriene CysLT2 receptor.";
RL   Biochem. Biophys. Res. Commun. 274:316-322(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20459128; PubMed=10851239;
RA   Heise C.E., O'Dowd B.F., Figueroa D.J., Sawyer N., Nguyen T.,
RA   Im D.-S., Stocco R., Bellefeuille J.N., Abramovitz M., Cheng R.,
RA   Williams D.L. Jr., Zeng Z., Liu Q., Ma L., Clements M.K., Coulombe N.,
RA   Liu Y., Austin C.P., George S.R., O'Neill G.P., Metters K.M.,
RA   Lynch K.R., Evans J.F.;
RT   "Characterization of the human cysteinyl leukotriene 2 receptor.";
RL   J. Biol. Chem. 275:30531-30536(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20345741; PubMed=11093801;
RA   Nothacker H.-P., Wang Z., Zhu Y., Reinscheid R.K., Lin S.H.S.,
RA   Civelli O.;
RT   "Molecular cloning and characterization of a second human cysteinyl
RT   leukotriene receptor: discovery of a subtype selective agonist.";
RL   Mol. Pharmacol. 58:1601-1608(2000).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Dunn M.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RT   "Identification of G protein-coupled receptor genes from the human
RT   genome sequence.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE OF 17-346 FROM N.A.
RA   Suga H.;
RT   "Homo sapiens cysteinyl leukotriene receptor 1 like receptor.";
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RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for cysteinyl leukotrienes. The response is
CC       mediated via a G-protein that activates a phosphatidylinositol-
CC       calcium second messenger system. Stimulation by BAY u9773, a
CC       partial agonist, induces specific contractions of pulmonary veins
CC       and might also have an indirect role in the relaxation of the
CC       pulmonary vascular endothelium. The rank order of affinities for
CC       the leukotrienes is LTC4 = LTD4 >> LTE4.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Widely expressed, with highest levels in the
CC       heart, placenta, spleen, peripheral blood leukocytes and adrenal
CC       gland. In lung, expressed in the interstitial macrophages, and
CC       slightly in smooth muscle cells.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB038269; BAB03601.1; -.
DR   EMBL; AF254664; AAG17291.1; -.
DR   EMBL; AF279611; AAK69485.1; -.
DR   EMBL; AL137118; CAC29102.1; -.
DR   EMBL; AB083603; BAB89316.1; -.
DR   EMBL; AB041644; BAB16379.1; -.
DR   Genew; HGNC:18274; CYSLTR2.
DR   MIM; 605666; -.
DR   GO; GO:0004974; F:leukotriene receptor activity; NAS.
DR   GO; GO:0030105; P:anaphylaxis; NAS.
DR   InterPro; IPR004071; Cysleuk_receptor.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR01533; CYSLTRECPTR.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN       1     42       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    43     63       1 (POTENTIAL).
FT   DOMAIN      64     72       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    73     93       2 (POTENTIAL).
FT   DOMAIN      94    123       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   124    144       3 (POTENTIAL).
FT   DOMAIN     145    153       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   154    174       4 (POTENTIAL).
FT   DOMAIN     175    204       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   205    225       5 (POTENTIAL).
FT   DOMAIN     226    245       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   246    266       6 (POTENTIAL).
FT   DOMAIN     267    286       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   287    307       7 (POTENTIAL).
FT   DOMAIN     308    346       CYTOPLASMIC (POTENTIAL).
FT   DISULFID   111    197       BY SIMILARITY.
FT   CARBOHYD    20     20       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    26     26       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    30     30       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   181    181       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   346 AA;  39635 MW;  EB54A4AIDDCE5E64 CRC64;

  Query Match          100.0%;  Score 1712;  DB 1;  Length 346;
  Best Local Similarity  100.0%;  Pred. No. 4.5e-99;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFWGVLGNGLSIYVFLQPYKKSTSVNVF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFWGVLGNGLSIYVFLQPYKKSTSVNVF 76

Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         77 MLNLAISDLLPISTLPFRADYFLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 136

Qy        121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSFQNGSVTSCLELNLYKIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSFQNGSVTSCLELNLYKIA 196

Qy        181 KLQTNMYIALVVVCCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLLIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 KLQTNMYIALVVVCCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLLIF 256

Qy        241 FLCFLPFHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACPNPLLYYFAGENFKDRL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 FLCFLPFHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACPNPLLYYFAGENFKDRL 316

Qy        301 KSALRKGHPQKAKTKCVFPVSVWLRKTRVV 330
              |||||||||||||||||||||||||||||
Db        317 KSALRKGHPQKAKTKCVFPVSVWLRKTRVV 346

RESULT 2
CLT2_PIG
ID   CLT2_PIG       STANDARD;      PRT:   345 AA.
AC   Q95N03;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Cysteinyl leukotriene receptor 2 (CysLTR2).
GN   CYSLTR2 OR CYSLT2.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kamohara M., Takasaki J., Matsumoto M., Matsumoto S., Saito T.,
RA   Ohishi T., Soga T., Matsushime H., Furuichi K.;
RT   "Characterization of the cloned rat and porcine cysteinyl leukotriene
RT   receptors.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for cysteinyl leukotrienes. The response is
CC       mediated via a G-protein that activates a phosphatidylinositol-
CC       calcium second messenger system (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB052662; BAB60817.1; -.
DR   InterPro; IPR004071; Cysleuk_receptor.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR01533; CYSLTRECPTR.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN       1     43       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    44     64       1 (POTENTIAL).
FT   DOMAIN      65     73       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    74     94       2 (POTENTIAL).
FT   DOMAIN      95    124       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   125    145       3 (POTENTIAL).
FT   DOMAIN     146    154       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   155    175       4 (POTENTIAL).
FT   DOMAIN     176    205       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   206    226       5 (POTENTIAL).
FT   DOMAIN     227    246       CYTOPLASMIC (POTENTIAL).
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FT   TRANSMEM    247    267       6 (POTENTIAL).
FT   DOMAIN      268    287       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    288    308       7 (POTENTIAL).
FT   DOMAIN      309    345       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    112    188       BY SIMILARITY.
FT   CARBOHYD     20     20       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     29     29       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    177    177       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    184    184       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   345 AA;  39410 MW;  5D1B1FB89BB95905 CRC64;

  Query Match             79.9%;  Score 1367.5;  DB 1;  Length 345;
  Best Local Similarity   79.2%;  Pred. No. 7.9e-78;
  Matches  262;  Conservative   24;  Mismatches   42;  Indels    3;  Gaps    2;

Qy          1 MEPNGTFSNNNS-RNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNV 59
                |||| |   |:|| |:|| ||||||:|||||:|| || |||| ||||||:|||||||||
Db         17 MEPNSTLGNHNSNRSCTTENFKREFYPIVYLVIFIWGALGNGFSIYVFLKPYKKSTSVNV 76

Qy         60 FMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVV 119
              |||||||||||   ||||| |||||||| ||||  |||||||:|||||||||||||||||
Db         77 FMLNLAISDLLFTITLPFRVDYYLRGSNXIFGDTPCRIMSYSMYVNMYSSIYFLTVLSVV 136

Qy        120 RFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKI 179
              |||| ||||||| |||::||||||:||| ||||| :|| :||||   :|| ||||| |:
Db        137 RFLATVHPFRLLHTTSIKNAWILCGVIWIFIMASSTVLLKNGSEQKDNVTLCLELNSNKV 196

Qy        180 AKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLII 239
               ||:||||:||||| :||| ||||||||||| |||||||||||:|||||| |:|| |||
Db        197 TKLKTMNYVALVVGFVLPFGTLSICYLLIIRALLKVEVPESGLRLSHRKALITVIIALII 256

Qy        240 FFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDR 299
               | ||||||| |||:|| ||    ||||||: :|||||||:|||| |||||||||||
Db        257 FLLCFLPYHVLRTLHLLEWKADKCKDRLHKAVAVTLALAAANSCFNPFLYYFAGENFKDR 316

Qy        300 LKSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
              |||||||| ||   ||:| | | |||:|||||
Db        317 LKSALRKGRPQ--KTRCGFSVCVWLKKETRV 345


RESULT 3
CLT2_MOUSE
ID   CLT2_MOUSE     STANDARD;      PRT;   309 AA.
AC   Q920A1;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Cysteinyl leukotriene receptor 2 (CysLTR2).
GN   CYSLTR2 OR CYSLT2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=21601669; PubMed=11591709;
RA   Hui Y., Yang G., Galczenski H., Figueroa D.J., Austin C.P.,
RA   Copeland N.G., Gilbert D.J., Jenkins N.A., Funk C.D.;
RT   "The murine cysteinyl leukotriene 2 (CysLT2) receptor. cDNA and
RT   genomic cloning, alternative splicing, and in vitro
RT   characterization.";
RL   J. Biol. Chem. 276:47489-47495(2001).
CC   -!- FUNCTION: Receptor for cysteinyl leukotrienes. The response is
CC       mediated via a G-protein that activates a phosphatidylinositol-
CC       calcium second messenger system. The rank order of affinities for
CC       the leukotrienes is LTC4 = LTD4 >> LTE4.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Widely expressed at low levels, with highest
CC       expression in the spleen, thymus and adrenal gland, and lower in
CC       the kidney, brain and peripheral blood leukocytes.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF331658; AAK97354.1; -.
DR   MGD; MGI:1917336; Cysltr2.
DR   GO; GO:0001631; F:cysteinyl leukotriene receptor activity; IDA.
DR   InterPro; IPR004071; Cysleuk_receptor.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR01533; CYSLTRECPTR.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN        1     26       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     27     47       1 (POTENTIAL).
FT   DOMAIN       48     56       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     57     77       2 (POTENTIAL).
FT   DOMAIN       78     98       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     99    119       3 (POTENTIAL).
FT   DOMAIN      120    138       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    139    159       4 (POTENTIAL).
FT   DOMAIN      160    187       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    188    208       5 (POTENTIAL).
FT   DOMAIN      209    229       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    230    250       6 (POTENTIAL).
FT   DOMAIN      251    271       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    272    292       7 (POTENTIAL).
FT   DOMAIN      293    309       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     95    171       BY SIMILARITY.
FT   CARBOHYD     14     14       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   309 AA;  35227 MW;  327B14A6EDDD2A02 CRC64;

  Query Match             69.9%;  Score 1197;  DB 1;  Length 309;
  Best Local Similarity   72.7%;  Pred. No. 2.2e-67;
  Matches  224;  Conservative   31;  Mismatches   53;  Indels    0;  Gaps    0;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 60
              ||   || |: ::|||||||||:||:||:||||||| |||| |||||||  ||||||||
Db          1 MEVTGTPSSYSNRNCTIENFKKEFYPIIYLIIFFWGALGNGFSIYVFLQTCKKSTSVNVF 60

Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
              |||| || ||||||||||||| |||||||||||||:|||||||||||:||||||||||||
Db         61 MLNLATSDFLFISTLPFRADYYFRGSNWIFGDLACRVMSYSLYVNMYTSIYFLTVLSVVR 120

Qy        121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
              | | |||||: ||||:|||||||||||: ||||| :|| :| |:  :: |||||:  |
Db        121 FQATVHPFRMFHVTSVRSAWILCGIIWVFIMASSALLLVNGQEEKDNIISCLELSPQKFK 180

Qy        181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIF 240
                |  ||:||: || |||| ||::|||||||:||| |:|||| | :||||||||:| :| |
Db        181 SLLIMNHIAVAVGFLLPFLTLTVCYLLIIRILLKAEIPESGPRAAHRKALTTIVIAMITF 240

Qy        241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
               |||||| |||:|| ||      | | |||| |||| :||||:|||| ||||||||| ||
Db        241 LLCFLPYHALRTLHLVTWDKDSCGDVLHKATVITLTMAAANSCFNPFLYYFAGENFKARL 300

Qy        301 KSALRKGH 308
               ::  | |
Db        301 RAIFSKVH 308


RESULT 4
CLT2_RAT
ID   CLT2_RAT       STANDARD;      PRT;   309 AA.
AC   Q924T9;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
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DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Cysteinyl leukotriene receptor 2 (CysLTR2) (RSBPT32).
GN   CYSLTR2 OR CYSLT2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kamohara M., Takasaki J., Matsumoto M., Matsumoto S., Saito T.,
RA   Ohishi T., Soga T., Matsushime H., Furuichi K.;
RT   "Characterization of the cloned rat and porcine cysteinyl leukotriene
RT   receptors.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for cysteinyl leukotrienes. The response is
CC       mediated via a G-protein that activates a phosphatidylinositol-
CC       calcium second messenger system (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
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CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AB052661; BAB60816.1; -.
DR   InterPro; IPR004071; Cysleuk_receptor.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR01533; CYSLTRECPTR.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN        1     26       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     27     47       1 (POTENTIAL).
FT   DOMAIN       48     56       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     57     77       2 (POTENTIAL).
FT   DOMAIN       78     98       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     99    119       3 (POTENTIAL).
FT   DOMAIN      120    137       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    138    158       4 (POTENTIAL).
FT   DOMAIN      159    187       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    188    208       5 (POTENTIAL).
FT   DOMAIN      209    229       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    230    250       6 (POTENTIAL).
FT   DOMAIN      251    271       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    272    292       7 (POTENTIAL).
FT   DOMAIN      293    309       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     95    171       BY SIMILARITY.
FT   CARBOHYD     14     14       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    166    166       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    167    167       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   309 AA;  35507 MW;  A122AC8177879D56 CRC64;

  Query Match             69.3%;  Score 1187;  DB 1;  Length 309;
  Best Local Similarity   73.1%;  Pred. No. 9.3e-67;
  Matches  225;  Conservative   26;  Mismatches   57;  Indels    0;  Gaps    0;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 60
                |    || |   :  :|||||||||:|:||:||||| || |||| ||||||| |||||||||
Db          1 MGVTGTPSYYSDKNCTIENFKRDFYPIIYLIIFVWGALGNGFSIYVFLQTYKKSTSVNVF 60

Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
              ||||||| |||||||||||   |||:||||| |||||||||||||:||||||||:||
Db         61 MLNLAISDFLFISTLPFRADYNFRGSDWIFGDWACRIMSYSLYVNMYTSIYFLTVLSIVR 120

Qy        121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
              |||  |||:: |:||:|||||||||||: ||||| :||  | |:  : | | |||| |
Db        121 FLATAHPFQMLHITSVRSAWILCGIIWVFIMASSGLLLKHGQEKKNNTTLCFELNLQKFK 180

Qy        181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIF 240
                |  :||||| || ||||| |:||||||||||||||:||||  | :  ||||||:| :|||
Db        181 NLVILNYIALGVGFLLPFFILTICYLLIIRVLLKVEIPESGPRDAQRKALTTIVIAMIIF 240

Qy        241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
                |||||| |||:|| ||     | | |||| |||| |||||:|||| ||||||||| ||
Db        241 LLCFLPYHALRTIHLVTWDADSCMDELHKATVITLTLAAANSCFNPFLYYFAGENFKARL 300

Qy        301 KSALRKGH 308
              ::   | |
Db        301 RAIFSKDH 308


RESULT 5
CLT1_RAT
ID   CLT1_RAT        STANDARD;      PRT;   339 AA.
AC   Q924T8;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Cysteinyl leukotriene receptor 1 (CysLTR1).
GN   CYSLTR1 OR CYSLT1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Takasaki J., Kamohara M., Saito T., Matsumoto M., Matsumoto S.,
RA   Ohishi T., Soga T., Matsushime H., Furuichi K.;
RT   "Characterization of cloned rat and porcine cysteinyl leukotriene
RT   receptors.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for cysteinyl leukotrienes mediating
CC       constriction of the microvascular smooth muscle during an
CC       inflammatory response. This response is mediated via a G-protein
CC       that activates a phosphatidylinositol-calcium second messenger
CC       system (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   --------------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AB052685; BAB60825.1; -.
DR   InterPro; IPR004071; Cysleuk_receptor.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR01533; CYSLTRECPTR.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN        1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     31     51       1 (POTENTIAL).
FT   DOMAIN       52     59       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     60     80       2 (POTENTIAL).
FT   DOMAIN       81    108       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    109    129       3 (POTENTIAL).
FT   DOMAIN      130    143       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    144    164       4 (POTENTIAL).
FT   DOMAIN      165    195       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    196    216       5 (POTENTIAL).
FT   DOMAIN      217    232       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    233    253       6 (POTENTIAL).
FT   DOMAIN      254    278       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    279    299       7 (POTENTIAL).
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FT   DOMAIN      300    339       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     98    175       BY SIMILARITY.
FT   CARBOHYD      6      6       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    171    171       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   339 AA;  39143 MW;  281B41DF050DF8EA CRC64;

  Query Match             33.1%;  Score 567.5;  DB 1;  Length 339;
  Best Local Similarity   36.7%;  Pred. No. 1.4e-28;
  Matches  122;  Conservative   70;  Mismatches  115;  Indels   25;  Gaps    8;

Qy          6 TFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSISVNVFMLNLA 65
              :||||   : ||: |: :  :  :| :|    |  ||    :|| :: | : ::  |:|:|||
Db         10 SFSNNRCHD-TIDEFRNQVYSTMYSMISVVGFFGNSFVLYVLIKTYHEKSAFQVYMINLA 68

Qy         66 ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMV 125
              |:||| : ||| |  ||:      | |||  ||: :|:||||:| ||:|:| :|  | :|:|
Db         69 IADLLCVCTLPLRVVYYVHKGKWFFGDFLCRLTTYALYVNLYCSIFFMTAMSFFRCVAIV 128

Qy        126 HPFRLLHVTSIRSAWILCGIIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--L 182
              | : ::: : : |  :|  ||| :|:| ||  ||     :     : | |  |     |  |  :
Db        129 FPVQNINLVTQKKARFVCVGIWIFVILTSSPFLLSKSYQDEKNNTKCFEPPQDKQTKKYV 188

Qy        183 QTMNYIALVVGCLLPFFILSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFL 242
              ::|::|: | ::|| |: :|| :|| |||  : ::     | |||: ||:     | :
Db        189 LVLHYVSLIFGFIIPFVTIIVCYTMIILTLLKNTMKKN--LPSRRKAIGMIIVVTAAFLV 246

Qy        243 CFLPYHTLRTVHL--TTWKVGLCKD--RLHKALVITLALAAANACFNPLLYYFAGENFKD 298
              |:|||  | :||        :    |      |: |::||||:|||:| ||:||||:|:| ||:
Db        247 SFMPYHIQRAIHLHFLHSETRSCDSVLRMQKSVVITLSLAASNCCFDPLLYFFSGGNFRR 306

Qy        299 RLKSALRK-------------GHPQKAKTKC 316
              || |  ||              |:|  :  |
Db        307 RL-STFRKHSLSSMTYIPKKKASLPEKGEEMC 337


RESULT 6
CLT1_PIG
ID   CLT1_PIG        STANDARD;      PRT;   340 AA.
AC   Q95N02;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Cysteinyl leukotriene receptor 1 (CysLTR1).
GN   CYSLTR1 OR CYSLT1.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Takasaki J., Kamohara M., Saito T., Matsumoto M., Matsumoto S.,
RA   Ohishi T., Soga T., Matsushime H., Furuichi K.;
RT   "Characterization of cloned rat and porcine cysteinyl leukotriene
RT   receptors.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for cysteinyl leukotrienes mediating
CC       constriction of the microvascular smooth muscle during an
CC       inflammatory response. This response is mediated via a G-protein
CC       that activates a phosphatidylinositol-calcium second messenger
CC       system (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AB052686; BAB60826.1; -.
DR   InterPro; IPR004071; Cysleuk_receptor.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR01533; CYSLTRECPTR.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN        1     31       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     32     52       1 (POTENTIAL).
FT   DOMAIN       53     60       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     61     81       2 (POTENTIAL).
FT   DOMAIN       82    109       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    110    130       3 (POTENTIAL).
FT   DOMAIN      131    144       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    145    165       4 (POTENTIAL).
FT   DOMAIN      166    196       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    197    217       5 (POTENTIAL).
FT   DOMAIN      218    233       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    234    254       6 (POTENTIAL).
FT   DOMAIN      255    279       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    280    300       7 (POTENTIAL).
FT   DOMAIN      301    340       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     99    176       BY SIMILARITY.
FT   CARBOHYD      6      6       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     18     18       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    172    172       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    265    265       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   340 AA;  38986 MW;  54F9372A121CE413 CRC64;

  Query Match             32.9%;  Score 563;  DB 1;  Length 340;
  Best Local Similarity   37.4%;  Pred. No. 2.6e-28;
  Matches  116;  Conservative   75;  Mismatches  101;  Indels   18;  Gaps    6;

Qy          8 SNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAIS 67
              :::|: | ||::|: : :  :| :|    |  |||  :|| :: | : ::  |:|:|||::
Db         12 ASSNTCNDTIDDFRNQVYSTLYSMITVVGFFGNGFVLYVLIKTYHEKSAYQVYMINLAVA 71

Qy         68 DLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHP 127
              ||| : ||| |  ||:      |:||| ||: :|:||||:| ||:|:| :|  | :|:| |
Db         72 DLLCVCTLPLRVVYYVHKGIWLFGDFLCRLSTYALYVNLYCSIFFMTAMSFFRCIAIVFP 131

Qy        128 FRLLHVTSIRSAWILCGIIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--LQT 184
              : ::: : : | |:|  ||| :|: ||  |: :   :   : | | |        ||  :
Db        132 VQNINLITHKKAKIVCIAIWIFVILTSSPFLMSTSYKDEKNNTKCFEPPQXNQAKYHVLV 191

Qy        185 MNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCF 244
              ::|::| || ::||  :|| :|| |||  : ::     | :||: ||:     | : |
Db        192 LHYVSLFVGFIIPFVIIIVCYTMIILTLLKNSMKKN--ISSRKKAIGMIIVVTAAFLISF 249

Qy        245 LPYHTLRTVHLTTWKVGLCKD--------RLHKALVITLALAAANACFNPLLYYFAGENF 296
              :|||  ||:||           |   |        |: |:: |||:|||:| ||:||||:|:| ||
Db        250 MPYHIQRTIHLHF----LHNDTKHCDSVLRMQKSVXITLSLAASNCCFDPLLYFFSGGNF 305

Qy        297 KDRLKSALRK 306
              :: |  |  ||
Db        306 REGL-STFRK 314


RESULT 7
CLT1_MOUSE
ID   CLT1_MOUSE      STANDARD;      PRT;   352 AA.
AC   Q99JA4; Q9JJ71; Q9JK47;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Cysteinyl leukotriene receptor 1 (CysLTR1) (Cysteinyl leukotriene D4
DE   receptor) (LTD4 receptor).
GN   CYSLTR1 OR CYSLT1 OR CYSLT1R.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
```

```
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC   STRAIN=129/Sv;
RX   PubMed=11226226;
RA   Maekawa A., Kanaoka Y., Lam B.K., Austen K.F.;
RT   "Identification in mice of two isoforms of the cysteinyl leukotriene 1
RT   receptor that result from alternative splicing.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:2256-2261(2001).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   STRAIN=C57BL/6; TISSUE=Trachea;
RX   MEDLINE=21562332; PubMed=11705452;
RA   Martin V., Sawyer N., Stocco R., Unett D., Lerner M.R., Abramovitz M.,
RA   Funk C.D.;
RT   "Molecular cloning and functional characterization of murine
RT   cysteinyl-leukotriene 1 (CysLT1) receptors.";
RL   Biochem. Pharmacol. 62:1193-1200(2001).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Blood;
RX   MEDLINE=21240338; PubMed=11342226;
RA   Mollerup J., Jorgensen S.T., Hougaard C., Hoffmann E.K.;
RT   "Identification of a murine cysteinyl leukotriene receptor by
RT   expression in Xenopus laevis oocytes.";
RL   Biochim. Biophys. Acta 1517:455-459(2001).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=T-cell;
RA   Ogasawara H., Izumi T., Shimizu T.;
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for cysteinyl leukotrienes mediating
CC       constriction of the microvascular smooth muscle during an
CC       inflammatory response. This response is mediated via a G-protein
CC       that activates a phosphatidylinositol-calcium second messenger
CC       system. The rank order of affinities for the leukotrienes is LTD4
CC       >> LTE4 = LTC4 >> LTB4.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1; Synonyms=Long;
CC         IsoId=Q99JA4-1; Sequence=Displayed;
CC       Name=2; Synonyms=Short;
CC         IsoId=Q99JA4-2; Sequence=VSP_001921;
CC   -!- TISSUE SPECIFICITY: Widely expressed, with higher expression in
CC       the lung and skin, intermediate levels in the heart, kidney and
CC       stomach and lower levels in several other tissues. Isoform 1 is
CC       the most abundant form in all tested tissues.
CC   -!- MISCELLANEOUS: MK-571, a selective antagonist, was shown to
CC       inhibit eosinophilia, bronchial hyperreactivity and microvascular
CC       leakage. Zafirlukast (Accolate) and pranlukast (Onon) were also
CC       shown to be selective antagonists.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF329272; AAK16715.1; -.
DR   EMBL; AF329272; AAK16716.1; -.
DR   EMBL; AF205830; AAK15433.1; -.
DR   EMBL; AF263370; AAF73047.1; -.
DR   EMBL; AB044087; BAA96809.1; -.
DR   HSSP; P34996; 1DDD.
DR   MGD; MGI:1926218; Cysltr1.
DR   GO; GO:0005887; C:integral to plasma membrane; IDA.
DR   GO; GO:0004974; F:leukotriene receptor activity; IDA.
DR   InterPro; IPR004071; Cysleuk_receptor.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR01533; CYSLTRECPTR.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Alternative splicing.
FT   DOMAIN        1     43       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     44     64       1 (POTENTIAL).
FT   DOMAIN       65     72       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     73     93       2 (POTENTIAL).
FT   DOMAIN       94    121       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    122    142       3 (POTENTIAL).
FT   DOMAIN      143    156       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    157    177       4 (POTENTIAL).
FT   DOMAIN      178    208       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    209    229       5 (POTENTIAL).
FT   DOMAIN      230    245       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    246    266       6 (POTENTIAL).
FT   DOMAIN      267    291       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    292    312       7 (POTENTIAL).
FT   DOMAIN      313    352       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    111    188       BY SIMILARITY.
FT   CARBOHYD     15     15       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     19     19       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     26     26       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    184    184       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC      1     13       Missing (in isoform 2).
FT                                /FTId=VSP_001921.
FT   CONFLICT    176    176       Y -> D (IN REF. 3).
SQ   SEQUENCE   352 AA;  40715 MW;  5BDC94B3F1CD0CAB CRC64;

  Query Match             32.7%;  Score 560;  DB 1;  Length 352;
  Best Local Similarity   38.5%;  Pred. No. 4.1e-28;
  Matches  117;  Conservative   69;  Mismatches  108;  Indels   10;  Gaps    6;

Qy         10 NNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDL 69
              ||: : ||: |: : :  :| :|   |  ||   :|| :: | : ::  |:|:||||:||
Db         26 NNTCHDTIDEFRNQVYSTMYSVISVVGFFGNSFVLYVLIKTYHEKSAFQVYMINLAIADL 85

Qy         70 LFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPFR 129
              | : ||| |  ||:    |:|||  ||: :|:||||:| ||:|:| :|  | :|:| | :
Db         86 LCVCTLPLRVVYYVHKGKWLFGDFLCRLTTYALYVNLYCSIFFMTAMSFFRCVAIVFPVQ 145

Qy        130 LLHVTSIRSAWILCGIIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--LQTMN 186
               ::: : : |  :|  ||| :|: || |:     :   : | | |      ||  :  ::
Db        146 NINLVTQKKARFVCIGIWIFVILTSSPFLMYKSYQDEKNNTKCFEPPQNNQAKKYVLILH 205

Qy        187 YIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFLP 246
              |::|  | ::|| |: :|| :||  |||  : ::    | |||:  ||:    | : |:|
Db        206 YVSLFFGFIIPFVTIIVCYTMIILTLLKNTMKKN--MPSRRKAIGMIIVVTAAFLVSFMP 263

Qy        247 YHTLRTVHLTTW--KVGLCKD--RLHKALVITLALAAANACFNPLLYYFAGENFKDRLKS 302
              ||  ||:||     :   |    |: |::||||:|||:| ||:||||:|:| ||: || |
Db        264 YHIQRTIHLHLLHSETRPCDSVLRMQKSVVITLSLAASNCCFDPLLYFFSGGNFRRRL-S 322

Qy        303 ALRK 306
                ||
Db        323 TFRK 326


RESULT 8
CLT1_HUMAN
ID   CLT1_HUMAN     STANDARD;      PRT;   337 AA.
AC   Q9Y271;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Cysteinyl leukotriene receptor 1 (CysLTR1) (Cysteinyl leukotriene D4
DE   receptor) (LTD4 receptor) (HG55) (HMTMF81).
GN   CYSLTR1 OR CYSLT1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
```

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RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Tonsil;
RX   MEDLINE=99318129; PubMed=10391245;
RA   Lynch K.R., O'Neill G.P., Liu Q., Im D.-S., Sawyer N., Metters K.M.,
RA   Coulombe N., Abramovitz M., Figueroa D.J., Zeng Z., Connolly B.M.,
RA   Bai C., Austin C.P., Chateauneuf A., Stocco R., Greig G.M.,
RA   Kargman S., Hooks S.B., Hosfield E., Williams D.L. Jr.,
RA   Ford-Hutchinson A.W., Caskey C.T., Evans J.F.;
RT   "Characterization of the human cysteinyl leukotriene CysLT1
RT   receptor.";
RL   Nature 399:789-793(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Leukocyte, Peripheral blood monocytes, and Spleen;
RX   MEDLINE=99393629; PubMed=10462554;
RA   Sarau H.M., Ames R.S., Chambers J., Ellis C., Elshourbagy N.,
RA   Foley J.J., Schmidt D.B., Muccitelli R.M., Jenkins O., Murdock P.R.,
RA   Herrity N.C., Halsey W., Sathe G., Muir A.I., Nuthulaganti P.,
RA   Dytko G.M., Buckley P.T., Wilson S., Bergsma D.J., Hay D.W.P.;
RT   "Identification, molecular cloning, expression, and characterization
RT   of a cysteinyl leukotriene receptor.";
RL   Mol. Pharmacol. 56:657-663(1999).
CC   -!- FUNCTION: Receptor for cysteinyl leukotrienes mediating
CC       bronchoconstriction of individuals with and without asthma.
CC       Stimulation by LTD4 results in the contraction and proliferation
CC       of smooth muscle, edema, eosinophil migration and damage to the
CC       mucus layer in the lung. This response is mediated via a G-protein
CC       that activates a phosphatidylinositol-calcium second messenger
CC       system. The rank order of affinities for the leukotrienes is LTD4
CC       >> LTE4 = LTC4 >> LTB4.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Widely expressed, with highest levels in
CC       spleen and peripheral blood leukocytes. Lower expression in
CC       several tissues, such as lung (mostly in smooth muscle bundles
CC       and alveolar macrophages), placenta, small intestine, pancreas,
CC       colon and heart.
CC   -!- MISCELLANEOUS: Selective antagonists, such as montelukast
CC       (Singulair), zafirlukast (Accolate) and pranlukast (Onon), are
CC       used in the treatment of the asthma crisis.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   --------------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF119711; AAD42285.1; -.
DR   EMBL; AF133266; AAD42778.1; -.
DR   HSSP; P34996; 1DDD.
DR   Genew; HGNC:17451; CYSLTR1.
DR   MIM; 300201; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005624; C:membrane fraction; TAS.
DR   GO; GO:0004974; F:leukotriene receptor activity; TAS.
DR   GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
DR   GO; GO:0006952; P:defense response; TAS.
DR   GO; GO:0007585; P:respiratory gaseous exchange; TAS.
DR   InterPro; IPR004071; Cysleuk_receptor.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR01533; CYSLTRECPTR.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN        1     28       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     29     49       1 (POTENTIAL).
FT   DOMAIN       50     57       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     58     78       2 (POTENTIAL).
FT   DOMAIN       79    106       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    107    127       3 (POTENTIAL).
FT   DOMAIN      128    141       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    142    162       4 (POTENTIAL).
FT   DOMAIN      163    193       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    194    214       5 (POTENTIAL).
FT   DOMAIN      215    230       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    231    251       6 (POTENTIAL).
FT   DOMAIN      252    276       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    277    297       7 (POTENTIAL).
FT   DOMAIN      298    337       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     96    173       BY SIMILARITY.
FT   CARBOHYD      6      6       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    169    169       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    180    180       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    262    262       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   337 AA;  38541 MW;  B9B53940F895F245 CRC64;

  Query Match             32.7%;  Score 559;  DB 1;  Length 337;
  Best Local Similarity   38.0%;  Pred. No. 4.5e-28;
  Matches  116;  Conservative   71;  Mismatches  106;  Indels   12;  Gaps    7;

Qy         11 NSRNC--TIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISD 68
              :|  |  ||::|: : : :| :|   |  |||  :|| :: | | :: |:|:|||::|
Db         10 SSATCHDTIDDFRNQVYSTLYSMISVVGFFGNGFVLYVLIKTYHKKSAFQVYMINLAVAD 69

Qy         69 LLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPF 128
              || : ||| |  ||:    |:||| ||: :|:|||||:| ||:|:| :|   | :|:| |
Db         70 LLCVCTLPLRVVYYVHKGIWLFGDFLCRLSTYALYVNLYCSIFFMTAMSFFRCIAIVFPV 129

Qy        129 RLLHVTSIRSAWILCGIIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--LQTM 185
              : ::: : : |  :|  ||| :|: ||  |:     :   : | | |        |  :  :
Db        130 QNINLVTQKKARFVCVGIWIFVILTSSPFLMAKPQKDEKNNTKCFEPPQDNQTKNHVLVL 189

Qy        186 NYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFL 245
              :|::| || ::||  : :|| :||  |||  : ::    ||:||:  |::     | : |:
Db        190 HYVSLFVGFIIPFVIIIVCYTMIILTLLKKSMKKN--LSSHKKAIGMIMVVTAAFLVSFM 247

Qy        246 PYHTLRTVHLTTW--KVGLCKD--RLHKALVITLALAAANACFNPLLYYFAGENFKDRLK 301
              |||  ||:||      :    |     |: |::|||:|||:| ||:||||:|:| ||: ||
Db        248 PYHIQRTIHLHFLHNETKPCDSVLRMQKSVVITLSLAASNCCFDPLLYFFSGGNFRKRL- 306

Qy        302 SALRK 306
              |  ||
Db        307 STFRK 311


RESULT 9
GP17_HUMAN
ID   GP17_HUMAN     STANDARD;      PRT;   367 AA.
AC   Q13304; Q9UDZ6; Q9UE21;
DT   01-NOV-1997 (Rel. 35, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Probable P2Y purinoceptor GPR17 (P2Y-like receptor) (R12).
GN   GPR17.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RX   MEDLINE=96145150; PubMed=8558062;
RA   Raport C.J., Schweickart V.L., Chantry D., Eddy R.L. Jr., Shows T.B.,
RA   Godiska R., Gray P.W.;
RT   "New members of the chemokine receptor gene family.";
RL   J. Leukoc. Biol. 59:18-23(1996).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC   TISSUE=Hippocampus;
RX   MEDLINE=98181695; PubMed=9523551;
RA   Blaesius R.H., Weber R.G., Lichter P., Ogilvie A.;
RT   "A novel orphan G protein-coupled receptor primarily expressed in the
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RT   brain is localized on human chromosomal band 2q21.";
RL   J. Neurochem. 70:1357-1365(1998).
CC   -!- FUNCTION: Putative receptor for purines coupled to G-proteins (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=Q13304-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q13304-2; Sequence=VSP_001987;
CC   -!- TISSUE SPECIFICITY: PRIMARILY EXPRESSED IN BRAIN.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   --------------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U33447; AAB16746.1; -.
DR   EMBL; Y12546; CAA73144.1; -.
DR   EMBL; Z94154; CAB08107.1; -.
DR   EMBL; Z94155; CAB08108.1; -.
DR   HSSP; P34996; 1DDD.
DR   Genew; HGNC:4471; GPR17.
DR   MIM; 603071; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0004950; F:chemokine receptor activity; TAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Alternative splicing.
FT   DOMAIN        1     64       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     65     85       1 (POTENTIAL).
FT   DOMAIN       86     92       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     93    113       2 (POTENTIAL).
FT   DOMAIN      114    133       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    134    154       3 (POTENTIAL).
FT   DOMAIN      155    175       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    176    196       4 (POTENTIAL).
FT   DOMAIN      197    223       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    224    244       5 (POTENTIAL).
FT   DOMAIN      245    260       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    261    281       6 (POTENTIAL).
FT   DOMAIN      282    308       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    309    329       7 (POTENTIAL).
FT   DOMAIN      330    367       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    132    209       BY SIMILARITY.
FT   CARBOHYD     42     42       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    204    204       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    282    282       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC      1     28       Missing (in isoform 2).
FT                                /FTId=VSP_001987.
SQ   SEQUENCE   367 AA;  40989 MW;  132FBE97BE83C60C CRC64;

  Query Match             28.0%;  Score 479;  DB 1;  Length 367;
  Best Local Similarity   34.8%;  Pred. No. 4.1e-23;
  Matches  112;  Conservative   62;  Mismatches  126;  Indels   22;  Gaps    9;

Qy          7 FSNNNSRNCTIEN-FKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA 65
              ||    :  |  |     :    |    ||: |    ::|| |::::|:: :|  |  |||:::||
Db         43 FSLATAEQCGQETPLENMLFASFYLLDFILALVGNTLALWLFIRDHKSGTPANVFLMHLA 102

Qy         66 ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMV 125
              ::||  :  || |  |:  |::| ||::|||:  :  |:|||:|||||| :|  ||||:|
Db        103 VADLSCVLVLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTCISADRFLAIV 162

Qy        126 HPFRLLHVTSIRSAWILCGIIWILI-MASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQT 184
              || : | :      | : |  :|::: :| : :|:    : |       ||:  ||:  |
Db        163 HPVKSLKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQ--LYR-EKASH 219

Qy        185 MNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHR---KALTTIIITLIIFF 241
               ::| |     || |    |||!||| |          ||||  |     ||:  | | | ||
Db        220 HALVSLAVAFTFPFITTVTCYLLIIRSL------RQGLRVEKRLKTKAVRMIAIVLAIFL 273

Qy        242 LCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYYFAGENFK 297
              :||:|||  |:|::  ::       |  :    ||    ||  | : |    :|::|:|  | |:
Db        274 VCFVPYHVNRSVYVLHYRSHGASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFR 333

Qy        298 DRLKSAL----RKGHPQKAKTK 315
                 | : |       || |    : |
Db        334 HALCNLLCGKRLKGPPPSFEGK 355


RESULT 10
P2YR_MELGA
ID   P2YR_MELGA     STANDARD;      PRT;   362 AA.
AC   P49652;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor) (6H1
DE   orphan receptor).
GN   P2RY1.
OS   Meleagris gallopavo (Common turkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX   NCBI_TaxID=9103;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=94335907; PubMed=8058061;
RA   Filtz T.M., Li Q., Boyer J.L., Nicholas R.A., Harden T.K.;
RT   "Expression of a cloned P2Y purinergic receptor that couples to
RT   phospholipase C.";
RL   Mol. Pharmacol. 46:8-14(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97382456; PubMed=9240460;
RA   Li Q., Schachter J.B., Harden T.K., Nicholas R.A.;
RT   "The 6H1 orphan receptor, claimed to be the p2y5 receptor, does not
RT   mediate nucleotide-promoted second messenger responses.";
RL   Biochem. Biophys. Res. Commun. 236:455-460(1997).
CC   -!- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
CC       ATP AND ADP. SEEMS TO MEDIATE ITS ACTION VIA A PERTUSSIS TOXIN
CC       INSENSITIVE G-PROTEIN, PROBABLY BELONGING TO THE GQ FAMILY THAT
CC       ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: MAINLY FOUND IN BLOOD, BRAIN, AND LUNG. TO A
CC       LESSER EXTENT IN STOMACH, GUT, AND SKELETAL MUSCLE.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; U09842; AAA18784.1; -.
DR   EMBL; AF012103; AAB65428.1; -.
DR   HSSP; P34996; 1DDD.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
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FT   DOMAIN        1     41       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     42     63       1 (POTENTIAL).
FT   DOMAIN       64     76       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     77     98       2 (POTENTIAL).
FT   DOMAIN       99    115       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    116    136       3 (POTENTIAL).
FT   DOMAIN      137    155       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    156    177       4 (POTENTIAL).
FT   DOMAIN      178    207       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    208    227       5 (POTENTIAL).
FT   DOMAIN      228    254       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    255    274       6 (POTENTIAL).
FT   DOMAIN      275    292       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    293    317       7 (POTENTIAL).
FT   DOMAIN      318    362       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    113    191       BY SIMILARITY.
FT   CARBOHYD     11     11       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     26     26       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    102    102       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    186    186       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   362 AA;  41180 MW;  3E128AB9EB64349C CRC64;

  Query Match             27.5%;  Score 470;  DB 1;  Length 362;
  Best Local Similarity   31.0%;  Pred. No. 1.4e-22;
  Matches   99;  Conservative   82;  Mismatches  112;  Indels   26;  Gaps    7;

Qy          5 GTFSNNNSRNCTI--ENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFML 62
                |  : | |  |::      |:  :  | ||:::|  | ||| ::|::|:    :   : ::|:|
Db         21 GWAAGNASTKCSLTKTGFQFYYLPTVYILVFITGFLGNSVAIWMFVFHMRPWSGISVYMF 80

Qy         63 NLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFL 122
              |||::| |:: |||      ||    ::|||||: |::   :   :||:| || ||| :|| |:
Db         81 NLALADFLYVLTLPALIFYYFNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISVHRYT 140

Qy        123 AMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLL---DSGSEQNGSVTSCLE------ 173
               :||| : |        ::|  :  ::| |::|    :|     :|  :| ::| | :
Db        141 GVVHPLKSLGRLKKKNAVYVSSLVWALVVAVIAPILFYSGTGVRRNKTIT-CYDTTADEY 199

Qy        174 LNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTI 233
               |  | :   : |   ::   :       ||   :   || ||:: |:  ::   | ||    ||:: :
Db        200 LRSYFVYSMCTTVFMFCI-----PFIVILGCYGLIVKALIYKDLDNSPLR---RKSIYLV 251

Qy        234 IITLIIFFLCFLPYHTLRTVHL------TTWKVGLCKDRLHKALVITLALAAANACFNPL 287
               || | :| : :||:| ::|::|          | ::     |:::      :|  ||: |:| :|:
Db        252 IIVLTVFAVSYLPFHVMKTLNLRARLDFQTPQMCAFNDKVYATYQVTRGLASLNSCVDPI 311

Qy        288 LYYFAGENFKDRLKSALRK 306
               ||: ||: |: ||  | ||
Db        312 LYFLAGDTFRRRLSRATRK 330


RESULT 11
P2YR_CHICK
ID   P2YR_CHICK     STANDARD;      PRT;   362 AA.
AC   P34996;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
GN   P2RY1.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=93285340; PubMed=8508924;
RA   Webb T.E., Simon J., Krishek B.J., Bateson A.N., Smart T.G.,
RA   King B.F., Burnstock G., Barnard E.A.;
RT   "Cloning and functional expression of a brain G-protein-coupled ATP
RT   receptor.";
RL   FEBS Lett. 324:219-225(1993).
RN   [2]
RP   3D-STRUCTURE MODELING.
RX   MEDLINE=97026278; PubMed=8872457;
RA   van Rhee A.M., Fischer B., van Galen P.J.M., Jacobson K.A.;
RT   "Modelling the P2Y purinoceptor using rhodopsin as template.";
RL   Drug Des. Discov. 13:133-140(1995).
CC   -!- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
CC       ATP AND ADP. SEEMS TO MEDIATE ITS ACTION VIA A PERTUSSIS TOXIN
CC       INSENSITIVE G-PROTEIN, PROBABLY BELONGING TO THE GQ FAMILY THAT
CC       ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: BRAIN, SPINAL CORD, GASTROINTESTINAL TRACT,
CC       SPLEEN AND LEG MUSCLE. IS NOT DETECTED IN THE HEART, LIVER,
CC       STOMACH, LUNG AND KIDNEY.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   --------------------------------------------------------------------------
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CC   modified and this statement is not removed.  Usage  by  and for commercial
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X73268; CAA51716.1; -.
DR   PIR; S33733; S33733.
DR   PDB; 1DDD; 11-JUL-96.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; 3D-structure.
FT   DOMAIN        1     41       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     42     63       1 (POTENTIAL).
FT   DOMAIN       64     76       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     77     98       2 (POTENTIAL).
FT   DOMAIN       99    115       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    116    136       3 (POTENTIAL).
FT   DOMAIN      137    155       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    156    177       4 (POTENTIAL).
FT   DOMAIN      178    207       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    208    227       5 (POTENTIAL).
FT   DOMAIN      228    254       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    255    274       6 (POTENTIAL).
FT   DOMAIN      275    292       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    293    317       7 (POTENTIAL).
FT   DOMAIN      318    362       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    113    191       BY SIMILARITY.
FT   CARBOHYD     11     11       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     26     26       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    102    102       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    186    186       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   HELIX        42     69
FT   HELIX        77    102
FT   HELIX       115    137
FT   HELIX       154    178
FT   HELIX       205    231
FT   HELIX       250    275
FT   HELIX       290    305
FT   TURN        306    307
FT   HELIX       308    320
SQ   SEQUENCE   362 AA;  41194 MW;  A806C88FB9514761 CRC64;

  Query Match             27.3%;  Score 467;  DB 1;  Length 362;
  Best Local Similarity   30.7%;  Pred. No. 2.2e-22;
  Matches   98;  Conservative   83;  Mismatches  112;  Indels   26;  Gaps    7;

Qy          5 GTFSNNNSRNCTI--ENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFML 62
                |  : | :  |::      |:  :  | ||:::|  | ||| ::|::|:    :   : ::|:|
Db         21 GWAAGNATTKCSLTKTGFQFYYLPTVYILVFITGFLGNSVAIWMFVFHMRPWSGISVYMF 80
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Qy         63 NLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFL 122
              |||::| |:: |||      ||    ::|||||: |::  :  :||:| || ||| :|| |:
Db         81 NLALADFLYVLTLPALIFYYFNKTDWIFGDVMCKLQRFIFHVNLYGSILFLICISVHRYT 140

Qy        123 AMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLL---DSGSEQNGSVTSCLE------ 173
               :||| : |      ::|  :  ::| |::|     :|     :|   :| ::| | :
Db        141 GVVHPLKSLGRLKKKNAVYVSSLVWALVVAVIAPILFYSGTGVRRNKTIT-CYDTTADEY 199

Qy        174 LNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTI 233
              |  |  :  :  |  ::  :       ||  :   || ||::  |:  ::  | ||   ||::  :
Db        200 LRSYFVYSMCTTVFMFCI-----PFIVILGCYGLIVKALIYKDLDNSPLR---RKSIYLV 251

Qy        234 IITLIIFFLCFLPYHTLRTVHL------TTWKVGLCKDRLHKALVITLALAAANACFNPL 287
              || | :| : :||:| ::|::|        | ::     |:::     :|   ||: |:| :|:
Db        252 IIVLTVFAVSYLPFHVMKTLNLRARLDFQTPQMCAFNDKVYATYQVTRGLASLNSCVDPI 311

Qy        288 LYYFAGENFKDRLKSALRK 306
              ||: ||: |: ||  | ||
Db        312 LYFLAGDTFRRRLSRATRK 330
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RESULT 12
P2Y5_CHICK

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ID   P2Y5_CHICK     STANDARD;      PRT;   308 AA.
AC   P32250;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   P2Y purinoceptor 5 (P2Y5) (Purinergic receptor 5) (6H1).
GN   P2RY5.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=T-cell;
RX   MEDLINE=93329058; PubMed=8393036;
RA   Kaplan M.H., Smith D.I., Sundick R.S.;
RT   "Identification of a G protein coupled receptor induced in activated
RT   T cells.";
RL   J. Immunol. 151:628-636(1993).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: INDUCED IN ACTIVATED T-CELLS.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; L06109; AAB06587.1; -.
DR   PIR; I50241; I50241.
DR   HSSP; P34996; 1DDD.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
KW   Palmitate.
FT   DOMAIN        1     16       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     17     43       1 (POTENTIAL).
FT   DOMAIN       44     52       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     53     76       2 (POTENTIAL).
FT   DOMAIN       77     89       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     90    109       3 (POTENTIAL).
FT   DOMAIN      110    130       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    131    151       4 (POTENTIAL).
FT   DOMAIN      152    178       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    179    206       5 (POTENTIAL).
FT   DOMAIN      207    224       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    225    250       6 (POTENTIAL).
FT   DOMAIN      251    269       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    270    289       7 (POTENTIAL).
FT   DOMAIN      290    308       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   LIPID       281    281       PALMITATE (BY SIMILARITY).
FT   DISULFID     86    165       POTENTIAL.
SQ   SEQUENCE   308 AA;  35597 MW;  4214E969633B6F7D CRC64;

  Query Match             26.1%;  Score 447;  DB 1;  Length 308;
  Best Local Similarity   35.4%;  Pred. No. 3.3e-21;
  Matches  105;  Conservative   53;  Mismatches  119;  Indels   20;  Gaps    8;

Qy         12 SRNCTIE-NFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLL 70
               | ||: | :||   :  |: ::|  |:: | ::||:|     |         :|||||||||
Db          3 SSNCSTEDSFKYTLYGCVFSMVFVLGLIANCVAIYIFTFTLKVRNETTTYMLNLAISDLL 62

Qy         71 FISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPFRL 130
              |: |||||  ||     || |||: |:|      | ||| || ||| :|| ||||:|||||
Db         63 FVFTLPFRI-YYFVVRNWPFGDVLCKISVTLFYTNMYGSILFLTCISVDRFLAIVHPFRS 121

Qy        131 LHVTSIRSAWILCGIIWILIMASSI---MLLDSGSEQNGSVTSCLELNLYKIAKLQTMNY 187
                : : |:| |:| :|| ::| |              :  :     :| | |  :      ::
Db        122 KTLRTKRNARIVCVAVWITVLAGSTPASFFQSTNRQNNTEQRTCFE-NFPESTWKTYLSR 180

Qy        188 IAL---VVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCF 244
              | :   :||  :|        |  :::| | |  :  |  ::| :| |   | : |:|| ||
Db        181 IVIFIEIVGFFIPLILNVTCSTMVLRTLNK-PLTLSRNKLSKKKVLKMIFVHLVIFCFCF 239

Qy        245 LPYH-------TLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGE 294
               :||:        :||    ||        :        :|| :| :| ||:|::||| :
Db        240 VPYNITLILYSLMRT---QTWINCSVVTAVRTMYPVTLCIAVSNCCFDPIVYYFTSD 293
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RESULT 13
P2YR_RAT

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ID   P2YR_RAT      STANDARD;      PRT;   373 AA.
AC   P49651;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   01-FEB-1996 (Rel. 33, Last annotation update)
DE   P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
GN   P2RY1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Insulinoma;
RX   MEDLINE=95298025; PubMed=7779087;
RA   Tokuyama Y., Hara M., Jones E.M.C., Fan Z., Bell G.I.;
RT   "Cloning of rat and mouse P2Y purinoceptors.";
RL   Biochem. Biophys. Res. Commun. 211:211-218(1995).
CC   -!- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
CC       ATP AND ADP. IN PANCREATIC ISLETS, MAY MEDIATE SOME OF THE EFFECTS
CC       OF EXTRACELLULAR ATP ON INSULIN SECRETION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN MUSCLE, HEART, LIVER, KIDNEY,
CC       LUNG, BRAIN, SPLEEN, BUT NOT IN TESTIS.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
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DR   EMBL; U22830; AAA91303.1; -.
DR   HSSP; P34996; 1DDD.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN        1     52       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     53     74       1 (POTENTIAL).
FT   DOMAIN       75     87       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     88    109       2 (POTENTIAL).
FT   DOMAIN      110    126       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    127    147       3 (POTENTIAL).
FT   DOMAIN      148    166       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    167    188       4 (POTENTIAL).
FT   DOMAIN      189    218       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    219    238       5 (POTENTIAL).
FT   DOMAIN      239    265       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    266    285       6 (POTENTIAL).
FT   DOMAIN      286    303       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    304    328       7 (POTENTIAL).
FT   DOMAIN      329    373       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    124    202       BY SIMILARITY.
FT   CARBOHYD     11     11       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     27     27       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    113    113       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    197    197       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   373 AA;  42321 MW;  6DDF676287B5E648 CRC64;

  Query Match             26.1%;  Score 447;  DB 1;  Length 373;
  Best Local Similarity   32.1%;  Pred. No. 3.8e-21;
  Matches  102;  Conservative   81;  Mismatches  109;  Indels   26;  Gaps    9;

Qy          6 TFSNNNSRNCTI--ENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLN 63
                | : ::|  | :    |:  : | ||:::|  | ||| ::|::|:   |  : ::|:| |
Db         33 TAAVSSSFRCALIKTGFQFYYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFN 92

Qy         64 LAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLA 123
              ||::| |:: |||     ||    ::|||||: |::  :  :||:| || ||| :|  |:
Db         93 LALADFLYVLTLPALIFYYFNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISAHRYSG 152

Qy        124 MVHPFRLLHVTSIRSAWILCGIIW-ILIMASSIMLLDSGS--EQNGSVTSCLE------L 174
              :|:| : |       ::|  :   ::| |:::| | :|  ||:   :| :|| | :     |
Db        153 VVYPLKSLGRLKKKNAIYVSVLVWLIVVVAISPILFYSGTGIRKNKTVT-CYDSTSDEYL 211

Qy        175 NLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTII 234
                | |  : |         : : | :|   :  || ||:| |:  ::  | ||    ||:: :|
Db        212 RSYFIYSMCT----TVAMFC-IPLVLILGCYGLIVRALIYKDLDNSPLR---RKSIYLVI 263

Qy        235 ITLIIFFLCFLPYHTLRTVHL------TTWKVGLCKDRLHKALVITLALAAANACFNPLL 288
              | | :| : ::|:| ::|::|       | ::     ||::    :|  ||: |:| :|:|
Db        264 IVLTVFAVSYIPFHVMKTMNLRARLDFQTPEMCDFNDRVYATYQVTRGLASLNSCVDPIL 323

Qy        289 YYFAGENFKDRLKSALRK 306
              |: ||: |: ||  | ||
Db        324 YFLAGDTFRRRLSRATRK 341


RESULT 14
P2YR_HUMAN
ID   P2YR_HUMAN     STANDARD;      PRT;   373 AA.
AC   P47900;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
GN   P2RY1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=96257237; PubMed=8666290;
RA   Leon C., Vial C., Cazenave J.-P., Gachet C.;
RT   "Cloning and sequencing of a human cDNA encoding endothelial P2Y1
RT   purinoceptor.";
RL   Gene 171:295-297(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96158962; PubMed=8579591;
RA   Ayyanathan K., Tania W., Harbansjit S., Raghbir A.S., Barnard E.A.,
RA   Kunapuli S.P.;
RT   "Cloning and chromosomal localization of the human P2Y1
RT   purinoceptor.";
RL   Biochem. Biophys. Res. Commun. 218:783-788(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96205320; PubMed=8630005;
RA   Janssens R., Communi D., Pirotton S., Samson M., Parmentier M.,
RA   Boeynaems J.M.;
RT   "Cloning and tissue distribution of the human P2Y1 receptor.";
RL   Biochem. Biophys. Res. Commun. 221:588-593(1996).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RA   Leon C., Vial C., Weber J., Cazenave J.-P., Gacher C.;
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 95-373 FROM N.A., FUNCTION, AND INHIBITION STUDIES.
RC   TISSUE=Platelet;
RX   MEDLINE=98113162; PubMed=9442040;
RA   Jin J., Daniel J.L., Kunapuli S.P.;
RT   "Molecular basis for ADP-induced platelet activation. II. The P2Y1
RT   receptor mediates ADP-induced intracellular calcium mobilization and
RT   shape change in platelets.";
RL   J. Biol. Chem. 273:2030-2034(1998).
CC   -!- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
CC       ATP AND ADP. IN PLATELETS BINDING TO ADP LEADS TO MOBILIZATION OF
CC       INTRACELLULAR CALCIUM IONS VIA ACTIVATION OF PHOSPHOLIPASE C, A
CC       CHANGE IN PLATELET SHAPE, AND PROBABLY TO PLATELET AGGREGATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- INDUCTION: REPRESSED BY THE P2Y1 RECEPTOR-SPECIFIC ANTAGONISTS
CC       A3P5PS, A3P5P AND A2P5P. THESE INHIBIT CALCIUM ION MOBILIZATION
CC       AND SHAPE CHANGE IN PLATELETS.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; Z49205; CAA89066.1; -.
DR   EMBL; U42030; AAA97873.1; -.
DR   EMBL; U42029; AAA97872.1; -.
DR   EMBL; S81950; AAB47091.1; -.
DR   EMBL; AJ006945; CAA07339.1; -.
DR   EMBL; AF018284; AAB94556.1; -.
DR   PIR; JC4737; JC4737.
DR   HSSP; P34996; 1DDD.
DR   Genew; HGNC:8539; P2RY1.
DR   MIM; 601167; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0004872; F:receptor activity; TAS.
DR   GO; GO:0007200; P:G-protein signaling, coupled to IP3 second . . .; TAS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Platelet;
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```
KW   Blood coagulation.
FT   DOMAIN        1     52       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     53     74       1 (POTENTIAL).
FT   DOMAIN       75     87       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     88    109       2 (POTENTIAL).
FT   DOMAIN      110    126       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    127    147       3 (POTENTIAL).
FT   DOMAIN      148    166       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    167    188       4 (POTENTIAL).
FT   DOMAIN      189    218       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    219    238       5 (POTENTIAL).
FT   DOMAIN      239    265       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    266    285       6 (POTENTIAL).
FT   DOMAIN      286    303       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    304    328       7 (POTENTIAL).
FT   DOMAIN      329    373       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    124    202       BY SIMILARITY.
FT   CARBOHYD     11     11       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     27     27       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    113    113       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    197    197       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    138    138       MISSING (IN REF. 1).
SQ   SEQUENCE   373 AA;  42071 MW;  4DC7C668B4145392 CRC64;

  Query Match             26.1%;  Score 446;  DB 1;  Length 373;
  Best Local Similarity   32.1%;  Pred. No. 4.4e-21;
  Matches  102;  Conservative   79;  Mismatches  111;  Indels   26;  Gaps   10;

Qy          6 TFSNNNSRNC--TIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLN 63
                | : ::|  |  |    |:  :  | ||:::|  | ||| ::|::|:    |  : ::|:| |
Db         33 TAAVSSSFKCALTKTGFQFYYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFN 92

Qy         64 LAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLA 123
              ||::| |:: ||      ||     :: |||||  |::  :  :||:| || ||| :| |:
Db         93 LALADFLYVLTLPALIFYYFNKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSG 152

Qy        124 MVHPFRLLHVTSIRSAWILCGIIW-ILIMASSIMLLDSGS--EQNGSVTSCLE------L 174
              :|:| : |      ::|  :  ::| |:::| | :|  ||:   :| ::| | :      |
Db        153 VVYPLKSLGRLKKKNAICISVLVWLIVVVAISPILFYSGTGVRKNKTIT-CYDTTSDEYL 211

Qy        175 NLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTII 234
                 | |  : |      : : | :|   :  || ||:| |:  ::  | ||   ||::  :|
Db        212 RSYFIYSMCT----TVAMFC-VPLVLILGCYGLIVRALIYKDLDNSPLR---RKSIYLVI 263

Qy        235 ITLIIFFLCFLPYHTLRTVHLTT----WKVGLC--KDRLHKALVITLALAAANACFNPLL 288
               | | :| : ::|:| ::|::|            :|     ||::     :|    ||: |:| :|:|
Db        264 IVLTVFAVSYIPFHVMKTMNLRARLDFQTPAMCAFNDRVYATYQVTRGLASLNSCVDPIL 323

Qy        289 YYFAGENFKDRLKSALRK 306
              |: ||: |: ||  | ||
Db        324 YFLAGDTFRRRLSRATRK 341


RESULT 15
P2YR_BOVIN
ID   P2YR_BOVIN     STANDARD;      PRT;   373 AA.
AC   P48042;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
GN   P2RY1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Aortic endothelium;
RX   MEDLINE=95352058; PubMed=7626079;
RA   Henderson D.J., Elliot D.G., Smith G.M., Webb T.E., Dainty I.A.;
RT   "Cloning and characterisation of a bovine P2Y receptor.";
RL   Biochem. Biophys. Res. Commun. 212:648-656(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Corpus callosum;
RX   MEDLINE=99064562; PubMed=9848096;
RA   Deng G., Matute C., Kumar C.K., Fogarty D.J., Miledi R.;
RT   "Cloning and expression of a P2y purinoceptor from the adult bovine
RT   corpus callosum.";
RL   Neurobiol. Dis. 5:259-270(1998).
CC   -!- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
CC       ATP AND ADP.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X87628; CAA60958.1; -.
DR   EMBL; U34041; AAC78275.1; -.
DR   PIR; JC4162; JC4162.
DR   HSSP; P34996; 1DDD.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN        1     52       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     53     74       1 (POTENTIAL).
FT   DOMAIN       75     87       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     88    109       2 (POTENTIAL).
FT   DOMAIN      110    126       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    127    147       3 (POTENTIAL).
FT   DOMAIN      148    166       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    167    188       4 (POTENTIAL).
FT   DOMAIN      189    218       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    219    238       5 (POTENTIAL).
FT   DOMAIN      239    265       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    266    285       6 (POTENTIAL).
FT   DOMAIN      286    303       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    304    328       7 (POTENTIAL).
FT   DOMAIN      329    373       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    124    202       BY SIMILARITY.
FT   CARBOHYD     11     11       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     27     27       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    113    113       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    197    197       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   373 AA;  42287 MW;  9270A7175C0BDA76 CRC64;

  Query Match             25.8%;  Score 442;  DB 1;  Length 373;
  Best Local Similarity   31.0%;  Pred. No. 7.8e-21;
  Matches   95;  Conservative   78;  Mismatches  109;  Indels   24;  Gaps    7;

Qy         16 TIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLLFISTL 75
                |   |:  :  |  ||:::|  | ||| ::|::|:    |  : ::|:| ||:|::| |:: ||
Db         45 TKTGFQFYYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTL 104

Qy         76 PFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPFRLLHVTS 135
              |      ||     ::|||||  |::  :  :||:| || ||| :|  |:  :|:| : |
Db        105 PALIFYYFNKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLK 164

Qy        136 IRSAWILCGIIWILIMASSIMLL---DSGSEQNGSVTSCLE------LNLYKIAKLQTMN 186
                ::|  :  ::|::::     :|     :|  :| ::| | :       |  | |  : |
Db        165 KKNAVYISVLVWLIVVVGISPILFYSGTGIRKNKTIT-CYDTTSDEYLRSYFIYSMCT-- 221

Qy        187 YIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFLP 246
                : :  | :|   :   || ||:| |:  ::  | ||   ||::  :|| | :| : ::|
Db        222 --TVAMFC-VPLVLILGCYGLIVRALIYKDLDNSPLR---RKSIYLVIIVLTVFAVSYIP 275
```

```
Qy        247 YRTLRTVHL------TTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
              :| ::|::|       |::       ||::      :|  ||: |:| :|:||: ||: |: ||
Db        276 FHVNKTMNLRARLDFQTPRMCAFNDKVYATVQVTRGLASLNSCVDPILTFLAGDTFRKRL 335

Qy        301 KSALRK 306
                 | ||
Db        336 SRATRK 341

Search completed: October 8, 2003, 08:28:46
Job time : 24 secs
```

```
                    GenCore version 5.1.6
           Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:          October  8, 2003, 08:26:59 ; Search time 97 Seconds
                                              (without alignments)
                                              877.911 Million cell updates/sec

Title:           US-09-991-225-2
Perfect score:   1712
Sequence:        1 MEPNGTFSNNNSRNCTIENF..........KAKTKCVFPVSVWLRKETRV 330

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters:      830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       SPTREMBL_23:*
                 1:  sp_archea:*
                 2:  sp_bacteria:*
                 3:  sp_fungi:*
                 4:  sp_human:*
                 5:  sp_invertebrate:*
                 6:  sp_mammal:*
                 7:  sp_mhc:*
                 8:  sp_organelle:*
                 9:  sp_phage:*
                 10:  sp_plant:*
                 11:  sp_rodent:*
                 12:  sp_virus:*
                 13:  sp_vertebrate:*
                 14:  sp_unclassified:*
                 15:  sp_rvirus:*
                 16:  sp_bacteriap:*
                 17:  sp_archeap:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1204	70.3	309	11	Q8R528	Q8r528 mus musculu
2	553	32.3	337	4	Q8IV19	Q8iv19 homo sapien
3	487.5	28.5	337	4	Q96P68	Q96p68 homo sapien
4	477	27.9	339	4	Q8N5S7	Q8n5s7 homo sapien
5	457	26.7	357	13	Q9DE05	Q9de05 raja erinac
6	453	26.5	361	13	Q90X57	Q90x57 xenopus lae
7	439	25.6	373	11	Q8BMJ5	Q8bmj5 mus musculu
8	436.5	25.5	344	11	Q8BMC0	Q8bmc0 mus musculu
9	425	24.8	370	11	Q8BKK1	Q8bkk1 mus musculu
10	424.5	24.8	374	13	O57466	O57466 meleagris g
11	421	24.6	370	11	Q8BLG2	Q8blg2 mus musculu
12	412.5	24.1	359	13	Q9PVY7	Q9pvy7 anguilla an
13	409.5	23.9	342	6	Q9GK76	Q9gk76 capra hircu
14	406.5	23.7	342	6	Q9TTY5	Q9tty5 bos taurus
15	399	23.3	341	11	Q8C017	Q8c017 mus musculu
16	398.5	23.3	342	6	Q9XSD4	Q9xsd4 sus scrofa
17	392	22.9	351	12	Q9DHV5	Q9dhv5 yaba-like d
18	389	22.7	355	11	Q9JLY8	Q9jly8 rattus norv
19	387.5	22.6	296	6	Q9TTY6	Q9tty6 canis famil
20	387.5	22.6	343	11	Q8C131	Q8c131 mus musculu
21	386.5	22.6	355	11	Q8BVW4	Q8bvw4 mus musculu
22	386	22.5	330	4	Q9BXA5	Q9bxa5 homo sapien
23	386	22.5	334	4	Q8TDQ8	Q8tdq8 homo sapien
24	386	22.5	355	6	Q9MYJ8	Q9myj8 callithrix
25	385	22.5	399	11	Q8R3I1	Q8r3i1 mus musculu
26	384	22.4	377	11	Q8BVF1	Q8bvf1 mus musculu
27	383.5	22.4	355	11	Q8BMH9	Q8bmh9 mus musculu
28	382.5	22.3	372	4	Q9H1C0	Q9h1c0 homo sapien
29	382	22.3	390	13	Q8QGQ4	Q8qgq4 carassius a
30	381.5	22.3	378	6	Q8HZR6	Q8hzr6 macaca mula
31	380.5	22.2	358	13	Q9YGC3	Q9ygc3 xenopus lae
32	378	22.1	351	11	Q9EQ16	Q9eq16 mus musculu
33	378	22.1	355	4	Q9BYX5	Q9byx5 homo sapien
34	377	22.0	352	6	Q9TV47	Q9tv47 cercopithec
35	377	22.0	385	11	Q9JK40	Q9jk40 mus musculu
36	374.5	21.9	363	4	Q8TDS4	Q8tds4 homo sapien
37	374	21.8	351	6	Q9MYJ9	Q9myj9 oryctolagus
38	374	21.8	351	11	Q9ERH5	Q9erh5 mus musculu
39	373.5	21.8	352	6	Q9TQX0	Q9tqx0 cercopithec
40	373.5	21.8	380	5	Q9NFV0	Q9nfv0 lymnaea sta
41	373.5	21.8	387	4	Q8NGE4	Q8nge4 homo sapien
42	373	21.8	328	11	Q9ERK9	Q9erk9 mus musculu
43	373	21.8	358	6	Q9N0M0	Q9n0m0 ovis aries
44	372.5	21.8	339	6	Q9TUU3	Q9tuu3 macaca mula
45	372.5	21.8	352	6	Q9TSQ7	Q9tsq7 cercopithec

ALIGNMENTS

```
RESULT 1
Q8R528
ID   Q8R528     PRELIMINARY;     PRT;   309 AA.
AC   Q8R528;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Cysteinyl leukotriene 2 receptor.
GN   CYSLTR2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ishii S.;
RT   "Mouse CysLT2 Gene.";
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB058930; BAB86881.1; -.
DR   MGD; MGI:1917336; Cysltr2.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   309 AA;  35226 MW;  96FACC6B8AF96974 CRC64;

  Query Match             70.3%;  Score 1204;  DB 11;  Length 309;
  Best Local Similarity   73.4%;  Pred. No. 1.8e-90;
  Matches  226;  Conservative   30;  Mismatches   52;  Indels    0;  Gaps    0;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 60
                ||  || |: ::|||||||||:||:||:|||||||| |||| |||||||  |||||||||
Db          1 MEVTGTPSSYSNRNCTIENFKKEFYPIIYLIIFFWGALGNGFSIYVFLQTCKKSTSVNVF 60

Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
              ||||| || |||||||||||| ||||||||||||:|||||||||:|||||||||||
Db         61 MLNLATSDFLFISTLPFRADYYFRGSNWIFGDLACRVMSYSLYVNMYTSIYFLTVLSVVR 120

Qy        121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
```

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                 ||| |||||: ||||:|||||||||||: ||||| :|| :| |:  :: |||||:  |
Db         121 FLATVHPFRMFHVTSVRSAWILCGIIWVFIMASSALLLVNGQEEKDNIISCLELSPQKFK 180

Qy         181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIF 240
                 |  ||:||: || |||| ||:||||||||:||| |:|||| | :|||||||||:| :| |
Db         181 SLLIMNHIAVAVGFLLPFLTLTICYLLIIRILLKAEIPESGPRAAHRKALTTIVIAMITF 240

Qy         241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
                |||||| |||:|| ||       | | |||| |||| :||||:|||| ||||||||| ||
Db         241 LLCFLPYHALRTLHLVTWDKDSCGDVLHKATVITLTMAAANSCFNPFLYYFAGENFKARL 300

Qy         301 KSALRKGH 308
               ::   | |
Db         301 RAIFSKVH 308
```

RESULT 2
Q8IV19

```
ID   Q8IV19      PRELIMINARY;      PRT;   337 AA.
AC   Q8IV19;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC035750; AAH35750.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   337 AA;  38486 MW;  B9B09CE0FD305245 CRC64;

  Query Match             32.3%;  Score 553;  DB 4;  Length 337;
  Best Local Similarity   37.7%;  Pred. No. 2.4e-37;
  Matches  115;  Conservative   71;  Mismatches  107;  Indels   12;  Gaps    7;

Qy          11 NSRNC--TIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISD 68
               :|  |  ||::|: : :  :| :|   |  |||  :|| :: | | ::  |:|:|||::|
Db          10 SSATCHDTIDDFRNQVYSTLYSMISVVGFFGNGFVLYVLIKTYHKKSAFQVYMINLAVAD 69

Qy          69 LLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPF 128
               || : ||| |  ||:       |:|||  ||: :|:||||:| ||:|:| :|  | :|:| |
Db          70 LLCVCTLPLRVVYYVHKGIWLFGDFLCRLSTYALYVNLYCSIFFMTAMSFFRCIAIVFPV 129

Qy         129 RLLHVTSIRSAWILCGIIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--LQTM 185
               : ::: : : |   :|  ||| :|: ||  |:     :    : | | |        |  :  :
Db         130 QNINLVTQKKARFVCVGIWIFVILTSSPFLMAKPQKDEKNNTKCFEPPQDNQTKNHVLVL 189

Qy         186 NYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFL 245
               :|::| || ::||  : :|| :|| |||  : ::      ||:||:  |::      | : |:
Db         190 HYVSLFVGFIIPFVIIIVCYTMIILTLLKKSMKKN--LSSHKKAIGMIMVVTAAFLVSFM 247

Qy         246 PYHTLRTVHLTTW--KVGLCKD--RLHKALVITLALAAANACFNPLLYYFAGENFKDRLK 301
               ||| ||:||     :     |      : |::||||:|||:| ||:||||:|:| ||: ||
Db         248 PYHIQRTIHLHFLHNETKPCDSVLTMQKSVVITLSLAASNCCFDPLLYFFSGGNFRKRL- 306

Qy         302 SALRK 306
                |  ||
Db         307 STFRK 311
```

RESULT 3
Q96P68

```
ID   Q96P68      PRELIMINARY;      PRT;   337 AA.
AC   Q96P68;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   G protein-coupled receptor GPR99 (Putative G-protein coupled receptor)
DE   (Seven transmembrane helix receptor).
GN   GPR80 OR GPCR OR GPR99.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21458557; PubMed=11574155;
RA   Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O.,
RA   Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
RT   "Discovery and mapping of ten novel G protein-coupled receptor
RT   genes.";
RL   Gene 275:83-91(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RT   "Identification of G protein-coupled receptor genes from the human
RT   genome sequence.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   PubMed=12098360;
RA   Wittenberger T., Hellebrand S., Munck A., Kreienkamp H.J.,
RA   Schaller H.C., Hampe W.;
RT   "GPR99, a new G protein-coupled receptor belonging to a new subgroup
RT   of nucleotide receptors.";
RL   BMC Genomics 3:17-17(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT   "Genome-wide discovery and analysis of human seven transmembrane helix
RT   receptor genes.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF411109; AAL26480.1; -.
DR   EMBL; AB083598; BAB89311.1; -.
DR   EMBL; AF370886; AAM76912.1; -.
DR   EMBL; AB065877; BAC06095.1; -.
DR   Genew; HGNC:4531; GPR80.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor; Transmembrane.
SQ   SEQUENCE   337 AA;  38251 MW;  6814EA0044756CE6 CRC64;

  Query Match             28.5%;  Score 487.5;  DB 4;  Length 337;
  Best Local Similarity   34.9%;  Pred. No. 5.2e-32;
  Matches  111;  Conservative   64;  Mismatches  114;  Indels   29;  Gaps   10;

Qy          14 NCTIEN--FKREFFPIVYLIIFFWGVLGNG--LSIYVF-LQPYKKSTSVNVFMLNLAISD 68
               ||| ||    |  : |::| |||  |  ||    :| |:| ::|:| ||    : ||||| :|
Db          23 NCTDENIPLKMHYLPVIYGIIFLVGFPGNAVVISTYIFKMRPWKSST---IIMLNLACTD 79

Qy          69 LLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPF 128
               ||::::|||   ||  | ||||||  |: : :| : |:|||| |||  |: |: ::||
Db          80 LLYLTSLPFLIHYYASGENWIFGDFMCKFIRFSFHFNLYSSILFLTCFSIFRYCVIIHPM 139

Qy         129 RLLHVTSIRSAWILCGIIWILIMASSI---MLLDSGSEQNGS----VTSCLELNLYKIAK 181
                  :  | | : | ::||: : : |        |: | :  | |      :||  ||| |
Db         140 SCFSIHKTRCAVVACAVVWIISLVAVIPMTFLITSTNRTNRSACLDLTSSDELNTIK--- 196

Qy         182 LQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFF 241
                 | |        ||   :::|| || |          :| |:   :||     |: |: |:
Db         197 --WYNLILTATTFCLPLVIVTLCYTTIIHTLTHGLQTDSCLK---QKARRLTILLLLAFY 251

Qy         242 LCFLPYHTLRTVHLTTWKVGL---CKDRLHKALVITLALAAANACFNPLLYYFAGENFKD 298
               :||||:| || : : :  : :    ::::|:| :::  ||| |    | |||     :||:
Db         252 VCFLPFHILRVIRIESRLLSISCSIENQIHEAYIVSRPLAALNTFGNLLLYVVVSDNFQQ 311
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```
Qy        299 RLKSALR---KGHPQKAK 313
              : | :|    |: ::||
Db        312 AVCSTVRCKVSGNLEQAK 329


RESULT 4
Q8N5S7
ID   Q8N5S7      PRELIMINARY;      PRT;   339 AA.
AC   Q8N5S7;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   G protein-coupled receptor 17.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain, and Lung;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC031653; AAH31653.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   339 AA;  37860 MW;  BB0CAFD0FC371D63 CRC64;

  Query Match             27.9%;  Score 477;  DB 4;  Length 339;
  Best Local Similarity   34.8%;  Pred. No. 3.8e-31;
  Matches  112;  Conservative   61;  Mismatches  127;  Indels   22;  Gaps    9;

Qy          7 FSNNNSRNCTIEN-FKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA 65
              ||   :  |  |   :   |   ||: |   ::|| |::: |:: :|  |  |||:::||
Db         15 FSLATAEQCGQETPLENMLFASFYLLDFILALVGNTLALWFFIRDHKSGTPANVFLMHLA 74

Qy         66 ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMV 125
              ::||  :  || |  |:  |::| ||::|||:  :  |:|||:|||||| :|  ||||:|
Db         75 VADLSCVLVLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTCISADRFLAIV 134

Qy        126 HPFRLLHVTSIRSAWILCGIIWILI-MASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQT 184
              || :  | :        | : |  :|::: :| : :|:    : |      ||:  ||:  |
Db        135 HPVKSLKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQ--LYR-EKASH 191

Qy        185 MNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHR---KALTTIIITLIIFF 241
                 ::| |     || |   ||||||| |             ||||  |     ||:  | | | ||
Db        192 HALVSLAVAFTFPFITTVTCYLLIIRSL------RQGLRVEKRLKTKAVRMIAIVLAIFL 245

Qy        242 LCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYYFAGENFK 297
              :||:|||  |:|::  ::     |  :    ||      ||   | : |    :|::|:|  | |:
Db        246 VCFVPYHVNRSVYVLHYRSHGASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFR 305

Qy        298 DRLKSAL----RKGHPQKAKTK 315
                 | : |      || |   : |
Db        306 HALCNLLCGKRLKGPPPSFEGK 327


RESULT 5
Q9DE05
ID   Q9DE05      PRELIMINARY;      PRT;   357 AA.
AC   Q9DE05;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   P2Y receptor.
OS   Raja erinacea (Little skate).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
OC   Rajiformes; Rajidae; Raja.
OX   NCBI_TaxID=7782;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20459151; PubMed=10900200;
RA   Dranoff J.A., O'Neill A.F., Franco A.M., Cai S.Y., Connolly G.C.,
RA   Ballatori N., Boyer J.L., Nathanson M.H.;
RT   "A primitive ATP receptor from the little skate Raja erinacea.";
RL   J. Biol. Chem. 275:30701-30706(2000).
DR   EMBL; AF242850; AAG42684.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   357 AA;  41239 MW;  14604EE15DCBDB41 CRC64;

  Query Match             26.7%;  Score 457;  DB 13;  Length 357;
  Best Local Similarity   29.0%;  Pred. No. 1.7e-29;
  Matches   97;  Conservative   87;  Mismatches  115;  Indels   36;  Gaps   10;

Qy         12 SRNCTI-ENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLL 70
              :: |:: : |:  :  ||:|:|:|  | :|| ::::|:   :   :|: ::| || ::||
Db         24 NKTCSLNKGFQFYYLPIMYIIVFVTGFIGNSVALWMFIFHMRPWSSITIYMFNLVLADLF 83

Qy         71 FISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPFRL 130
              :: :||    ||   ::||||:| |::  :  :||:| || ||| :|| |:  :||| :
Db         84 YVFSLPILIFYYFNKTDWIFGELLCKLXRFIFHVNLYGSILFLTCISVHRYTGVVHPMKS 143

Qy        131 LHVTSIRSAWILCGIIWILIMA--SSIMLLDSGSEQNGSVTSCLE------LNLYKIAKL 182
              |    :|| |:|  :|| :||  | |:          :     :| :       |  |  |  :
Db        144 LGRLKKKSATIVCVCVWITVMAGISPILYFSRTGLRRNKTNTCYDTTSKELLETYFIYSM 203

Qy        183 QTMNYIALVVGCLLPFFTLSICYLLIIRVLLK--VEVPESGLRVSHRKALTTIIITLIIF 240
              |  :        |  :|| |: :||  |:: |:    :: |  |          |::  :|| | :|
Db        204 STTFF-----GFCIPFATILVCYGFIVKALISNDMKTPLRG------KSVRLVIIVLAVF 252

Qy        241 FLCFLPYHTLRTVHLTT--WKVGL--CK--DRLHKALVITLALAAANACFNPLLYYFAGE 294
               : :||:| :: ::| :   :  ||  |:   |::    :|  ||: |:| :|:||: ||:
Db        253 AISYLPFHVMKNLNLQSRLYYQGLDTCEWNRRVYATYQVTRGLASLNSCVDPILYFLAGD 312

Qy        295 NFKDRLKSALRKGHPQKAKTKCVF--------PVS 321
               |: |  :|  :    ::::      |          |||
Db        313 TFRRRFTNAASRFMTRRSELSMQFRSEDSPLQPVS 347


RESULT 6
Q90X57
ID   Q90X57      PRELIMINARY;      PRT;   361 AA.
AC   Q90X57;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   P2Y1 nucleotide receptor.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cheng A.W., Tsim K.W.;
RT   "Cloning of Xenopus P2Y1 Receptor.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF432354; AAL27614.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   361 AA;  41002 MW;  E5B2D605F5B57FED CRC64;
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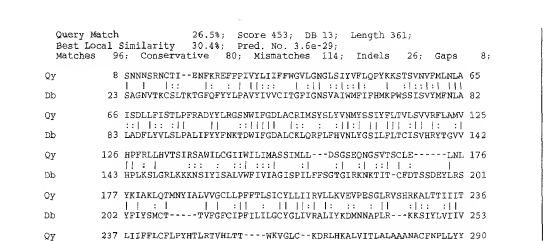
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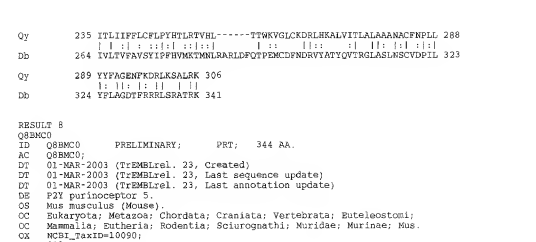
Matches 96; Conservative 80; Mismatches 114; Indels 26; Gaps 8;
Qy 8 SNNNSRNCTI--ENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQFYKKSTSVNVFMLNLA 65
Db 23 SAGNVTKCSLTKTGPGFYYLPAVIIVVCITGPIGNSVAIWMFIPHMKPWSSISVYMFNLA 82
Qy 66 ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYTVMYSSIYFLTVLSVVRFLAMV 125
Db 83 LADLFLVLTLPALIFYYFNKTDWIFGDALCKLQRFLPHVNLYGSILFLTCISVHRYTQVV 142
Qy 126 HPFRLLHVTSIRSAWILCGIIWILIMASSIMLL---DSGSEQNGSVTSCLE------LNL 176
Db 143 HPLKSLGRLKKKNSIYISALVWFIVIAGISPILFFSGTGIRKNKTIT-CFDTSSDEYLRS 201
Qy 177 YKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVSVPESGLRVSHRKALTTIIIT 236
Db 202 YPIYSMCT----TVFGFCIPFILILGCYGLIVRALIYKDMNNAPLR---KKSIYLVIIV 255
Qy 237 LIIFFLCPLFVHTLRTVHLTT----WKVGLC--KDRLHKALVITLALAAANACFNPLLYY 290
Db 254 LTVFAVSYLPFHVMKLNLRARLDFQSPEMCNFNDRVYATYQVTRGLASLNSCVDPILYF 313
Qy 291 FAGENFKDRLKSALRK 306
Db 314 LAGDTFRRKLSRATRK 329
RESULT 7
Q8BMJ5
ID Q8BMJ5 PRELIMINARY; PRT; 373 AA.
AC Q8BMJ5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE P2Y purinoceptor 1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Body;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK030759; BAC27125.1; -.
SQ SEQUENCE 373 AA; 42228 MW; BA88124B7847287C CRC64;
Query Match 25.6%; Score 439; DB 11; Length 373;
Best Local Similarity 30.5%; Pred. No. 5.2e-28;
Matches 97; Conservative 84; Mismatches 111; Indels 26; Gaps 8;
Qy 6 TPSNNNSRNC--TIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQFYKKSTSVNVFMLN 63
Db 33 TAAVSSSFOCALTKTGPQFYYLPAVYILVFIIGFLGNSVAIWMYVFHMKPWSGISVYMFN 92
Qy 64 LAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLA 123
Db 93 LALADFLYVLTLPALIFYYFNKTDWIFGDAMCKLQRFIPHVNLYGSILFLTCISAHRYSG 152
Qy 124 MVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLL---DSGSEQNGSVTSCLE------L 174
Db 153 VVYPLKSLGRLKKKNAIYVSVLVWLIVVVAISPILFYSGTGIRKNKTVT-CTLTTSNDLL 211
Qy 175 NLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVSVPESGLRVSHRKALTTII 234
Db 212 RSYPIYSMCT----TVAMPC-IPLVLILGCYGLIVRALIYNDLDNSPLR---KKSIYLVI 263


Qy 235 ITLIIFFLCPLFVHTLRTVHL------TTWKVGLCKDRLHKALVITLALAAANACFNPLL 288
Db 264 IVLTVFAVSYIPFHVMKTMNLRARLDFQTPEMCDFNDRVYATYQVTRGLASLNSCVDPIL 323
Qy 289 YYFAGENFKDRLKSALRK 306
Db 324 YPLAGDTFRRRLSRATRK 341
RESULT 8
Q8BMC0
ID Q8BMC0 PRELIMINARY; PRT; 344 AA.
AC Q8BMC0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE P2Y purinoceptor 5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mesonephros;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK032901; BAC38077.1; -.
SQ SEQUENCE 344 AA; 39438 MW; 50270D1D14AEDAB2 CRC64;
Query Match 25.5%; Score 436.5; DB 11; Length 344;
Best Local Similarity 32.4%; Pred. No. 7.7e-28;
Matches 100; Conservative 72; Mismatches 114; Indels 23; Gaps 8;
Qy 8 SNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQFYKKSTSVNVFMLNLAIS 67
Db 3 SSNGSQCPYDDSFKYTLYGCMFSMVFVLGLISNCVAIYIFICALKVRNETTTYMINLAMS 62
Qy 68 DLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHP 127
Db 63 DLLFVFTLPFFI-FYFAVRNWPFGDLLCKISVMLFYTNMYGSILFLTCISVDRFLAIVFP 121
Qy 128 FRLLHVTSIRSAWILCGIIWILIM---ASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQT 184
Db 122 FKSTLRTKRNAIIVCIAVWFTVWGGSAPVFFGSTSEQGNNTSSACFE--NFPAATWKT 179
Qy 185 -MNYIAL--YVGCLLPFFTLSICYLLIIRVLLKVSVPESGLRVSHRKALTTIIITLIIF 240
Db 180 YLSRIVIFIRIVGFFIPLLLNVICSSMVLRTLNK-PVTLSRSKMNKTXVLKMIFVHLVIP 238
Qy 241 PLCFLPVFHLRTVHLTTWKVGLCKDRLHKALV--------ITLALAAANACFNPLLYYFA 292
Db 239 CFCFVPYN----TNLILYSLMRTQTFVNCSVVAAVRTMPFITLCIAVSNCCFDPIVYYFT 294
Qy 293 GENFKDRLK 301
Db 295 SDTIQNSTK 303
RESULT 9
Q8BKK1
ID Q8BKK1 PRELIMINARY; PRT; 370 AA.
AC Q8BKK1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE P2Y purinoceptor 9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Dorsal root ganglion;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK051709; BAC34729.1; -.
SQ   SEQUENCE   370 AA;  41956 MW;  AB126B42343AE6E1 CRC64;

  Query Match             24.8%;  Score 425;  DB 11;  Length 370;
  Best Local Similarity   31.7%;  Pred. No. 7.1e-27;
  Matches  103;  Conservative   68;  Mismatches  134;  Indels   20;  Gaps    9;

Qy          5 GTFSNNNSRNCTI-ENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLN 63
                | : ||:  | : ::||     || ::|  |:: |  |::||     |  :    :|: |
Db         23 GNATTNNT--CIVDDSFKYNLNGAVYSVVFILGLITNSASLFVFCFRMKMRSETAIFITN 80

Qy         64 LAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLA 123
              ||:|||||: ||||:  :|     :| |||  |:|    :   |:| |: ||| :|| ||||
Db         81 LALSDLLFVCTLPFKI-FYNFNRHWPFGDTLCKISGTAFLTNIYGSMLFLTCISVDRFLA 139

Qy        124 MVHPFRLLHVTSIRSAWILCGIIWILIMASSIML-LDSGSEQNGSVTSCLELNLYKIAK- 181
              :|:|||    : : |:: |:|  :|||::  |      | | :   | :  |:| |     :: |
Db        140 IVYPFRSRTIRTRRNSAIVCAGVWILVLNGGISASLFSTTNVNNATTTCFEGFSKRVWKT 199

Qy        182 -LQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIF 240
               |  :       ||| ::|      |   :::| | |       | :  :  :| |  | : : :|
Db        200 YLSKITIFIEVVGFIIPLILNVSCSSVVLRTLRK-PATLSQIGTNKKKVLKMITVHMAVF 258

Qy        241 FLCFLPYHTLRTVHLTTWKVGLCK---DRLHKALV-ITLALAAANACFNPLLYYFAGENF 296
               :||:||:::  ::            :      :|  | :  ||| ||  | ||:| :|||  |:|
Db        259 VVCFVPYNSVLFLYALVRSQAITNCLLERFAKIMYPITLCLATLNCCFDPFIYYFTLESF 318

Qy        297 KD--------RLKSALRKGHPQKAK 313
               :         |::|  :   |   |
Db        319 QKSFYINTHIRMESLFKTETPLTPK 343


RESULT 10
O57466
ID   O57466      PRELIMINARY;      PRT;   374 AA.
AC   O57466;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   G protein coupled P2Y nucleotide receptor.
GN   TP2Y.
OS   Meleagris gallopavo (Common turkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX   NCBI_TaxID=9103;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=98086419; PubMed=9415702;
RA   Boyer J.L., Waldo G.L., Harden T.K.;
RT   "Molecular cloning and expression of an avian G protein-coupled P2Y
RT   receptor.";
RL   Mol. Pharmacol. 52:928-934(1997).
DR   EMBL; AF031897; AAC60339.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   374 AA;  42594 MW;  849C465722BDD02B CRC64;

  Query Match             24.8%;  Score 424.5;  DB 13;  Length 374;
  Best Local Similarity   31.0%;  Pred. No. 7.9e-27;
  Matches   96;  Conservative   77;  Mismatches  112;  Indels   25;  Gaps    9;

Qy         18 ENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLLFISTLPF 77
              | ||     || | |:|  |:  |  ::::|:    :   :   :| ||||||  |:: :||
Db         37 EEFKFILLPISYGIVFVVGLPLNSWAMWIFVSRMRPWNATTTYMFNLAISDTLYVFSLPT 96

Qy         78 RADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIR 137
                  ||    :|| || : |:|: :  | |:|||| ||| :|| |:: : || | |      :
Db         97 LVYYYADRNNWPFGKVFCKIVRFLFYANLYSSILFLTCISVHRYMGICHPIRSLKWVKTK 156

Qy        138 SAWILCGIIWILI---MASSIMLLDSGSEQNGSV----TSCLELNLYKIAKLQTMNYIAL 190
              | ::|  :|:::   :   :::  : :  |: | ::     |     | : |          ::| :
Db        157 HARLICVGVWLVVTICLIPNLIFVTTSSKDNSTLCHDTTKPEEFDHY-------VHYSSS 209

Qy        191 VVGCL--LPFFTLSICYLLIIRVLLKVEVPESGLRV-SHRK-ALTTIIITLIIFFLCFLP 246
              ::  |  :||  : :||  |: : | |    |      || |::| ::  ||| | :| :||:|
Db        210 IMALLFGIPFLVIVVCYCLMAKRLCKRSFPSPSPRVPSYKKRSIKMIIIVLTVFAICFVP 269

Qy        247 YHTLRTVHLTT-WKVGLCK--DRLHKALVITLALAAANACFNPLLYYFAGENFKDRLKSA 303
              :|  ||:: |: :      |:  : ::      ||  ||: |:| :|:||: ||: :: |
Db        270 FHITRTLYYTSRYFQADCQTLNIINFTYKITRPLASINSCLDPILYFMAGDKYRGR---- 325

Qy        304 LRKGHPQKAK 313
              ||:|  |: :
Db        326 LRRGAAQRPR 335


RESULT 11
Q8BLG2
ID   Q8BLG2      PRELIMINARY;      PRT;   370 AA.
AC   Q8BLG2;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   P2Y purinoceptor 9.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK045289; BAC32299.1; -.
SQ   SEQUENCE   370 AA;  41872 MW;  0E4C79FEDFD32050 CRC64;

  Query Match             24.6%;  Score 421;  DB 11;  Length 370;
  Best Local Similarity   31.4%;  Pred. No. 1.5e-26;
  Matches  102;  Conservative   70;  Mismatches  133;  Indels   20;  Gaps    9;

Qy          5 GTFSNNNSRNCTI-ENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLN 63
                | : ||:  | : ::||     || ::|  |:: :  |::||     |  :    :|: |
Db         23 GNATANNT--CIVDDSFKYNLNGAVYSVVFILGLITSSASLFVFCFRMKMRSETAIFITN 80

Qy         64 LAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLA 123
              ||:|||||: ||||:  :|     :| |||  |:|    :   |:| |: ||| :|| ||||
Db         81 LALSDLLFVCTLPFKI-FYNFNRHWPFGDTLCKISGTAFLTNIYGSMLFLTCISVDRFLA 139

Qy        124 MVHPFRLLHVTSIRSAWILCGIIWILIMASSIML-LDSGSEQNGSVTSCLELNLYKIAK- 181
              :|:|||    : : |:: |:|  :|||::  |      | | :   | :  |:| |     :: |
Db        140 IVYPFRSRTIRTRRNSAIVCAGVWILVLSGGISASLFSTTNVNNATTTCFEGFSKRVWKT 199

Qy        182 -LQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIF 240
               |  :       ||| ::|      |   :::| | |       | :  :  :| |  | : : :|
Db        200 YLSKITIFIEVVGFIIPLILNVSCSSVVLRTLRK-PATLSQIGTNKKKVLKMITVHMAVF 258

Qy        241 FLCFLPYHTLRTVHLTTWKVGLCK---DRLHKALV-ITLALAAANACFNPLLYYFAGENF 296
```

```
                  :||:||::: ::         :      :|  | :  ||| ||  | ||:| :||| |:|
Db        259 VVCFVPYNSVLFLYALVRSQAITNCLLERFAKIMYPITLCLATLNCCFDPFIYYFTLESF 318

Qy        297 KD--------RLKSALRKGHPQKAK 313
              :         |::|  :   |   |
Db        319 QKSFYINTHIRMESLFKTETPLTPK 343


RESULT 12
Q9PVY7
ID   Q9PVY7      PRELIMINARY;      PRT;   359 AA.
AC   Q9PVY7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Angiotensin receptor.
OS   Anguilla anguilla (European freshwater eel).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC   Anguilla.
OX   NCBI_TaxID=7936;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Tran Van Chuoi M., Dolphin C.T., Barker S., Clark A.J., Vinson G.P.;
RT   "Molecular cloning and characterization of the cDNA encoding the
RT   angiotensin II recpetor of european eel Anguilla anguilla.";
RL   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AJ005132; CAB40835.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR006025; Zn_MTpeptdse.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
DR   PROSITE; PS00142; ZINC_PROTEASE; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   359 AA;  39997 MW;  053726AEA827C271 CRC64;

  Query Match             24.1%;  Score 412.5;  DB 13;  Length 359;
  Best Local Similarity   33.2%;  Pred. No. 7.2e-26;
  Matches  101;  Conservative   55;  Mismatches  123;  Indels   25;  Gaps    6;

Qy         26 PIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYLRG 85
              |:||   |  |::|| : : |      |   |  |:|:||||:||| |: |||   | :   |
Db         30 PVVYGCNFVIGIVGNSMVVAVIYCYMKLKTVANIFVLNLAVSDLTFLITLPMWATFTAMG 89

Qy         86 SNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILCGI 145
                || ||    |:    :       |:|:||:|||  ||: |:||:|||  |        ::  |  |  |  :
Db         90 YNWPFGGFLCKASAGLTIFNLYTSIFFLTSLSIDRYLAIVHPVRSRQRRTVVYARITCVL 149

Qy        146 IW---ILIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK-LQTMNYIALVVGCLLPFFTL 201
              ||     |:    :  :    |    :   :   :  |  |   |:  ::::   |    :    :    |:|  |:||   :
Db        150 IWAFAFLLSLPTALSRDVFTINHPNTTVCGTLDKHELSHVLVAIGLMKSVLGFLIPFVII 209

Qy        202 SICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVG 261
                || || |  ||:       :|  |       :  |   :     ::  ||||::|:          :|:      :
Db        210 VTCYCLIGRALLEARRVQSS-RSRGDEVLQMLAAVVLAFFLCWVPHQIFHFMHV----LA 264

Qy        262 LCK--------DRLHKALVITLALAAANACFNPLLYYFAGENFKDRL--------KSALR 305
              |  |             |  :   ||   |: :|   |:|  ||:||  |  |  ||:   |                  ||  |
Db        265 LLKVIENCPTLDIIDTALPFTICIAYFNSCMNPILYGFVGRNFRRNLLRLLRCGPGSAAR 324

Qy        306 KGHP 309
                ||
Db        325 HSHP 328


RESULT 13
Q9GK76
ID   Q9GK76      PRELIMINARY;      PRT;   342 AA.
AC   Q9GK76;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Platelet-activating factor receptor.
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Capra.
OX   NCBI_TaxID=9925;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yang W., Diehl J.R., Piumi F.;
RT   "Partial Sequence of Caprine Platelet-Activating Factor Receptor
RT   Gene.";
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF302764; AAG39982.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   342 AA;  39612 MW;  39D9379AED60FD4E CRC64;

  Query Match             23.9%;  Score 409.5;  DB 6;  Length 342;
  Best Local Similarity   30.3%;  Pred. No. 1.2e-25;
  Matches  100;  Conservative   64;  Mismatches  139;  Indels   27;  Gaps    9;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVF--LQPYKKSTSVN 58
              |||| :|  ::              |:    |||  | |:|  ||: |     ::||   |  |  ||     :
Db          1 MEPNNSFRVDS-------EFRYTLFPIFYSIVFVLGVIANSYVLWVFARLYPSKKFNEIK 53

Qy         59 VFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSV 118
              :||:||  ::||||: |||       ||        :||          |  :         ::|  |  |:  || |::
Db         54 IFMVNLTMADLLFLVTLPLWIVYYYNQGDWILPKFLCNLAGCFFFINTYCSVAFLAVITY 113

Qy        119 VRFLAMVHPFRLLHVTSIRSAWILCGIIWILIM--ASSIMLLDSGSEQ-----NGSVTSC 171
               || |:   |  :       |: :   ::|   |||: |:  ||     :||| :  :          :|::| |
Db        114 NRFQAVTRPIKTAQATTRKRGFLLSLIIWVSIVGAASYFFVLDSTNSEPKKTGSGNITRC 173

Qy        172 LELNLYKIAKLQTM-NYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKAL 230
                 |     |:     :     :    :| ||       |  |    :    |  |:||| ||   :|                 |:||
Db        174 FE--HYEKGSIPVLIIHIFLVFSFFLVFLIILFCNLVIIRTLLTQQVQMQRNAEVKRRAL 231

Qy        231 TTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKAL----VITLALAAANACFNP 286
                :    | :| :||:|:| :: :   |  ::|           |: :         :|| |  : |    :|
Db        232 WMVCTVLAVFVICFVPHHLVQ-LPWTLAELGFQDTDFHQGINDAHQVTLCLLSTNCVLDP 290

Qy        287 LLYYFAGENFKDRLKSALRKGHPQKAKTKC 316
              ::| |   : |:   |     |     :    :      ||
Db        291 IIYCFLTKKFRKHLTEKL---YSMRESRKC 317


RESULT 14
Q9TTY5
ID   Q9TTY5      PRELIMINARY;      PRT;   342 AA.
AC   Q9TTY5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Platelet-activating factor receptor.
GN   PAFR.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yang W.S., Diehl J.R., Roudebush W.E.;
RT   "Partial Sequence of Bovine Platelet-Activating Factor Receptor
```

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RT   Gene.";
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   He B., Tiemann U., Kanitz W., Weikard R., Laurent P., Schwerin M.,
RA   Schmidt P.;
RT   "Molecular characterization of bovine platelet-actvating factor
RT   receptor transcripts and their detection in different tissues of
RT   cattle.";
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF187321; AAF01439.2; -.
DR   EMBL; AJ295321; CAC43290.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   342 AA;  39691 MW;  7C4236205AE937C9 CRC64;

  Query Match             23.7%;  Score 406.5;  DB 6;  Length 342;
  Best Local Similarity   30.3%;  Pred. No. 2.1e-25;
  Matches  100;  Conservative   63;  Mismatches  140;  Indels   27;  Gaps    9;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVF--LQPYKKSTSVN 58
Db          1 MEPNNSFRVDS-------EFRYTLFPIFYSIVFVLGVIANSYVLWVFARLYPSKKFNEIK 53

Qy         59 VFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSV 118
Db         54 IFMVNLTMADLLFLVTLPLWIVYYYNQGDWILPKFLCNLAGCFFFINTYCSVAFLAVITY 113

Qy        119 VRFLAMVHPFRLLHVTSIRSAWILCGIIWILIM--ASSIMLLDSGSEQ-----NGSVTSC 171
Db        114 NRFQAVTRPIKTAQATTRKRGILLSLIIWVSIVGAASYFFVLDSTNREPNKTGSANITRC 173

Qy        172 LELNLYKIAKLQTMN-YIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKAL 230
Db        174 FE--HYEKGSIPVLTIHIFLVFSFFLVFLIILFCNLVIIRTLLTQQVQIQRNAEVKRRAL 231

Qy        231 TTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKAL----VITLALAAANACFNP 286
Db        232 WMVCTVLAVFIICFVPHHLVQ-LPWTLAELGFQDTDFHQAINDAHQVTLCLLSTNCVLDP 290

Qy        287 LLYYFAGENFKDRLKSALRKGHPQKAKTKC 316
Db        291 IIYCFLTKKFRKHLTEKL---YSMRESRKC 317


RESULT 15
Q8C017
ID   Q8C017      PRELIMINARY;      PRT;   341 AA.
AC   Q8C017;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Platelet activating factor receptor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK032547; BAC27919.1; -.
SQ   SEQUENCE   341 AA;  39175 MW;  25F97C6472797386 CRC64;

  Query Match             23.3%;  Score 399;  DB 11;  Length 341;
  Best Local Similarity   30.5%;  Pred. No. 8.7e-25;
  Matches  101;  Conservative   66;  Mismatches  134;  Indels   30;  Gaps   10;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVF--LQPYKKSTSVN 58
Db          1 MEHNGSFRVDS-------EFRYTLFPIVYSVIFILGVVANGYVLWVFANLYPSKKLNEIK 53

Qy         59 VFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSV 118
Db         54 IFMVNLTMADLLFLITLPLWIVYYYNEGDWILPNFLCNVAGCLFFINTYCSVAFLGVITY 113

Qy        119 VRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGS-------EQNGSVTSC 171
Db        114 NRYQAVAYPIKTAQATTRKRGISLSLIIWVSIVATASYFLATDSTNLVPNKDGSGNITRC 173

Qy        172 LE-LNLYKIAKLQTMNYIALVVGC-LLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKA 229
Db        174 FEHYEPYRGPILVVHVFIAF---CFFLVFFLIFYCNLVIIHTLLTQPMRQQRKAGVKRRA 230

Qy        230 LTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKAL----VITLALAAANACFN 285
Db        231 LWMVCTVLAVFIICFVPHHVVQ-LPWTLAELGY-QTNFHQAINDAHQITLCLLSTNCVLD 288

Qy        286 PLLYYFAGENFKDRLKSALRKGHPQKAKTKC 316
Db        289 PVIYCFLTKKFRKHLS---EKFYSMRSSRKC 316


Search completed: October  8, 2003, 08:30:34
Job time : 102 secs
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GenCore version 5.1.6

QM protein - protein search, using sw model

Run on: October 8, 2003, 08:26:59 ; Search time 21 Seconds
(without alignments)
664.885 Million cell updates/sec

Title: US-09-991-225-2
Perfect score: 1712
Sequence: 1 MEPNGTFSNNNSRNCTIENF.....KAKTKCVFPVSVWLRKETRV 330

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1703	99.5	346	4	US-09-585-876-2	Sequence 2, Appli
2	559	32.7	337	3	US-09-044-404A-2	Sequence 2, Appli
3	559	32.7	337	4	US-09-586-924-2	Sequence 2, Appli
4	479	28.0	339	1	US-08-153-848-44	Sequence 44, Appl
5	479	28.0	339	2	US-08-812-871-3	Sequence 3, Appli
6	479	28.0	339	3	US-09-299-843A-44	Sequence 44, Appl
7	479	28.0	339	4	US-09-088-337B-44	Sequence 44, Appl
8	479	28.0	339	4	US-09-170-496D-32	Sequence 32, Appl
9	479	28.0	339	5	PCT-US93-11153-44	Sequence 44, Appl
10	479	28.0	339	5	PCT-US95-07180-2	Sequence 2, Appli
11	476	27.8	339	4	US-09-170-496D-182	Sequence 182, App
12	461	26.9	362	3	US-08-513-974B-374	Sequence 374, App
13	442	25.8	373	2	US-08-559-524A-4	Sequence 4, Appli
14	442	25.8	373	3	US-08-749-707-4	Sequence 4, Appli
15	440	25.7	361	1	US-08-383-750-4	Sequence 4, Appli
16	440	25.7	361	3	US-08-352-678-4	Sequence 4, Appli
17	440	25.7	361	4	US-09-536-954-4	Sequence 4, Appli
18	440	25.7	361	4	US-09-170-496D-78	Sequence 78, Appl
19	440	25.7	361	5	PCT-US93-09636-4	Sequence 4, Appli
20	439.5	25.7	348	3	US-08-852-824-17	Sequence 17, Appl
21	439	25.6	302	2	US-08-467-948A-30	Sequence 30, Appl
22	439	25.6	302	3	US-08-467-947A-30	Sequence 30, Appl
23	437	25.5	344	2	US-08-467-948A-8	Sequence 8, Appli
24	437	25.5	344	3	US-08-467-947A-8	Sequence 8, Appli
25	434	25.4	361	4	US-09-170-496D-206	Sequence 206, App
26	430	25.1	370	3	US-08-749-707-2	Sequence 2, Appli
27	419.5	24.5	374	4	US-09-102-710B-3	Sequence 3, Appli
28	416.5	24.3	373	3	US-08-513-974B-373	Sequence 373, App
29	416	24.3	342	3	US-08-988-876-9	Sequence 9, Appli
30	416	24.3	375	1	US-08-442-134A-2	Sequence 2, Appli
31	416	24.3	375	1	US-08-444-581B-2	Sequence 2, Appli
32	416	24.3	375	1	US-08-446-088A-2	Sequence 2, Appli
33	416	24.3	375	2	US-08-559-524A-3	Sequence 3, Appli
34	416	24.3	375	3	US-08-749-707-3	Sequence 3, Appli
35	406.5	23.7	398	1	US-08-097-938-6	Sequence 6, Appli
36	406.5	23.7	398	1	US-08-476-000-6	Sequence 6, Appli
37	406.5	23.7	398	1	US-08-472-840-6	Sequence 6, Appli
38	406.5	23.7	398	2	US-08-476-976-6	Sequence 6, Appli
39	406.5	23.7	398	3	US-08-474-410-6	Sequence 6, Appli
40	405.5	23.7	398	3	US-08-486-673B-6	Sequence 6, Appli
41	405	23.7	355	3	US-09-045-583-53	Sequence 53, Appl
42	405	23.7	355	4	US-09-534-185-53	Sequence 53, Appl
43	401	23.4	347	4	US-08-405-271A-24	Sequence 24, Appl
44	400.5	23.4	398	1	US-08-097-938-4	Sequence 4, Appli
45	400.5	23.4	398	1	US-08-476-000-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-585-876-2
; Sequence 2, Application US/09585876
; Patent No. 6586205
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 43239, A No. 6586205el GPCR-Like Molecule and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 5800-88
; CURRENT APPLICATION NUMBER: US/09/585,876
; CURRENT FILING DATE: 2000-06-01
; EARLIER APPLICATION NUMBER: 60/182,061
; EARLIER FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-585-876-2

Query Match 99.5%; Score 1703; DB 4; Length 346;
Best Local Similarity 99.4%; Pred. No. 2.1e-124;
Matches 328; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MEPNGTFSNNNSRNCTIENFKREFPPIYVLIIFPWGVLGNGLSIYVFLQPYKKSTSVNVF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 MEPNGTFSNNNSRNCTIENFKREFPPIYVLIIFPWGVLGNGLSIYVFLQPYKKSTSVNVF 76

Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 MLNLAISDLLFISTLPFRADYYLRGSSWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 136

Qy        121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIVASSIMLDSGSEQNGSVTSCLELNLYKIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 FLAMVHPFRLLHVISIRSAWILCGIIWILIMASSIMLDSGSEQNGSVTSCLELNLYKIA 196

Qy        181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPEGGLRVSHRKALTTIITLIIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPEGGLRVSHRKALTTIITLIIF 256

Qy        241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLVLAAANACFNPLLYYFAGENFKDRL 316

Qy        301 KSALRKGHDPQEAKTKCVFPVSVWLRKETRV 330
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Db        317 KSALRKGHDPQEAKTKCVFPVSVWLRKETRV 346
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```
RESULT 2
US-09-044-404A-2
; Sequence 2, Application US/09044404A
; Patent No. 6200775
;  GENERAL INFORMATION:
;    APPLICANT:  SATHE, GANESH
;    APPLICANT:  HALSEY, WENDY
;    APPLICANT:  ELLIS, CATHERINE
;    APPLICANT:  AMES, ROBERT
;    APPLICANT:  FOLEY, JAMES
;    APPLICANT:  SARAU, HENRY
;    TITLE OF INVENTION:  cDNA CLONE HMTMF81 THAT ENCODES
;    TITLE OF INVENTION:  A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SmithKline Beecham Corporation
;      STREET:  790 Swedeland Road, P.O. Box 1539
;      CITY:  King of Prussia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19406
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/044,404A
;      FILING DATE:  MARCH 19, 1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/844,795
;      FILING DATE:  APRIL 22, 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Han, William T.
;      REGISTRATION NUMBER:  34,344
;      REFERENCE/DOCKET NUMBER:  GH-70001-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-270-5219
;      TELEFAX:  610-270-5090
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  337 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-044-404A-2

  Query Match             32.7%;  Score 559;  DB 3;  Length 337;
  Best Local Similarity   38.0%;  Pred. No. 4.5e-36;
  Matches  116;  Conservative   71;  Mismatches  106;  Indels   12;  Gaps    7;

Qy         11 NSRNC--TIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISD 68
              :|  |  ||::|: : :  :| :|    |  |||  :|| :: | | ::  |:|:|||::|
Db         10 SSATCHDTIDDFRNQVYSTLYSMISVVGFFGNGFVLYVLIKTYHKKSAFQVYMINLAVAD 69

Qy         69 LLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPF 128
              || : ||| |  ||:     |:|||  ||: :|:||||:| ||:|:| :|  | :|:| |
Db         70 LLCVCTLPLRVVYYVHKGIWLFGDFLCRLSTYALYVNLYCSIFFMTAMSFFRCIAIVFPV 129

Qy        129 RLLHVTSIRSAWILCGIIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--LQTM 185
              : ::: : : |  :|  ||| :|: || |:     :     : | | |        |  :  :
Db        130 QNINLVTQKKARFVCVGIWIFVILTSSPFLMAKPQKDGKNNTKCFEPPQDNQTKNHVLVL 189

Qy        186 NYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFL 245
              :|::| || ::||  : :|| :||  |||   : ::    ||:||:  |::     | : |:
Db        190 HYVSLFVGFIIPFVIIIVCYTMIILTLLKKSMKKN--LSSHKKAIGMIMVVTAAFLVSFM 247

Qy        246 PYHTLRTVHLTTW--KVGLCKD--RLHKALVITLALAAANACFNPLLYYFAGENFKDRLK 301
              |||  ||:||       :    |     |: |::||||:|||:| ||:||||:|:| ||: ||
Db        248 PYHIQRTIHLHFLHNETKPCDSVLRMQKSVVITLSLAASNCCFDPLLYFFSGGNFRKRL- 306

Qy        302 SALRK 306
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Db        307 STFRK 311


RESULT 3
US-09-586-924-2
; Sequence 2, Application US/09586924
; Patent No. 6506878
; GENERAL INFORMATION:
;  APPLICANT:  SATHE, GANESH M.
;  APPLICANT:  HALSEY, WENDY
;  APPLICANT:  ELLIS, CATHERINE E.
;  APPLICANT:  AMES, ROBERT S.
;  APPLICANT:  FOLEY, JAMES J.
;  APPLICANT:  SARAU, HENRY M.
;  APPLICANT:  CHAMBERS, JON
;  TITLE OF INVENTION:  cDNA CLONE HMTMF81 THAT ENCODES A NOVEL
;  TITLE OF INVENTION:  HUMAN 7-TRANSMEMBRANE RECEPTOR
;  FILE REFERENCE:  GH-70001-1D1
;  CURRENT APPLICATION NUMBER: US/09/586,924
;  CURRENT FILING DATE:  2000-06-05
;  PRIOR APPLICATION NUMBER:  09/044,404
;  PRIOR FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  08/844,795
;  PRIOR FILING DATE:  1997-04-22
;  NUMBER OF SEQ ID NOS:  2
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 337
;   TYPE: PRT
;   ORGANISM: HOMO SAPIENS
US-09-586-924-2

  Query Match             32.7%;  Score 559;  DB 4;  Length 337;
  Best Local Similarity   38.0%;  Pred. No. 4.5e-36;
  Matches  116;  Conservative   71;  Mismatches  106;  Indels   12;  Gaps    7;

Qy         11 NSRNC--TIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISD 68
              :|  |  ||::|: : :  :| :|    |  |||  :|| :: | | ::  |:|:|||::|
Db         10 SSATCHDTIDDFRNQVYSTLYSMISVVGFFGNGFVLYVLIKTYHKKSAFQVYMINLAVAD 69

Qy         69 LLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPF 128
              || : ||| |  ||:     |:|||  ||: :|:||||:| ||:|:| :|  | :|:| |
Db         70 LLCVCTLPLRVVYYVHKGIWLFGDFLCRLSTYALYVNLYCSIFFMTAMSFFRCIAIVFPV 129

Qy        129 RLLHVTSIRSAWILCGIIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--LQTM 185
              : ::: : : |  :|  ||| :|: || |:     :     : | | |        |  :  :
Db        130 QNINLVTQKKARFVCVGIWIFVILTSSPFLMAKPQKDGKNNTKCFEPPQDNQTKNHVLVL 189

Qy        186 NYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFL 245
              :|::| || ::||  : :|| :||  |||   : ::    ||:||:  |::     | : |:
Db        190 HYVSLFVGFIIPFVIIIVCYTMIILTLLKKSMKKN--LSSHKKAIGMIMVVTAAFLVSFM 247

Qy        246 PYHTLRTVHLTTW--KVGLCKD--RLHKALVITLALAAANACFNPLLYYFAGENFKDRLK 301
              |||  ||:||       :    |     |: |::||||:|||:| ||:||||:|:| ||: ||
Db        248 PYHIQRTIHLHFLHNETKPCDSVLRMQKSVVITLSLAASNCCFDPLLYFFSGGNFRKRL- 306

Qy        302 SALRK 306
              |  ||
Db        307 STFRK 311


RESULT 4
US-08-153-848-44
; Sequence 44, Application US/08153848
; Patent No. 5759804
;  GENERAL INFORMATION:
;    APPLICANT:  Godiska, Ronald
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Schweikart, Vicki L.
```

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;    TITLE OF INVENTION:  No. 5759804el Seven Transmembrane Receptors
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/153,848
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/977,452
;      FILING DATE:  17-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5759804and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  31794
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  339 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-153-848-44

  Query Match             28.0%;  Score 479;  DB 1;  Length 339;
  Best Local Similarity   34.8%;  Pred. No. 6.8e-30;
  Matches  112;  Conservative   62;  Mismatches  126;  Indels   22;  Gaps    9;

Qy          7 FSNNNSRNCTIEN-FKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA 65
                ||    :  |  |     :    |      ||: |     ::|| |::::|:: :|   |   |||:::||
Db         15 FSLATAEQCGQETPLENMLFASFYLLDFILALVGNTLALWLFIRDHKSGTPANVFLMHLA 74

Qy         66 ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMV 125
              ::||   :   ||  |   |:   |::|  ||::|||:   :   |:|||:||||| :|   ||||:|
Db         75 VADLSCVLVLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTCISADRFLAIV 134

Qy        126 HPFRLLHVTSIRSAWILCGIIWILI-MASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQT 184
              || : | :        | : |   :|::: :| : :|:     : |          ||:  ||:   |
Db        135 HPVKSLKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQ--LYR-EKASH 191

Qy        185 MNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHR---KALTTIIITLIIFF 241
                 ::| |     || |    ||||||| |              ||||   |      ||:   |  |  |  ||
Db        192 HALVSLAVAFTFPFITTVTCYLLIIRSL------RQGLRVEKRLKTKAVRMIAIVLAIFL 245

Qy        242 LCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYYFAGENFK 297
              :||:|||   |:|::   ::     .   |    :      ||      ||     |  :  |     :|::|:|   |  |:
Db        246 VCFVPYHVNRSVYVLHYRSHGASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFR 305

Qy        298 DRLKSAL----RKGHPQKAKTK 315
                |  :  |         ||  |      :  |
Db        306 HALCNLLCGKRLKGPPPSFEGK 327

RESULT 5
US-08-812-871-3
; Sequence 3, Application US/08812871
; Patent No. 5955303
;  GENERAL INFORMATION:
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Guegler, Karl
;    APPLICANT:  Muzong Cheng
;    TITLE OF INVENTION:  NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE
;    TITLE OF INVENTION:  PROTEIN
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Dr.
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/812,871
;      FILING DATE:  Filed Herewith
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0237 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  339 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  992700
US-08-812-871-3

  Query Match             28.0%;  Score 479;  DB 2;  Length 339;
  Best Local Similarity   34.8%;  Pred. No. 6.8e-30;
  Matches  112;  Conservative   62;  Mismatches  126;  Indels   22;  Gaps    9;

Qy          7 FSNNNSRNCTIEN-FKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA 65
                ||    :  |  |     :    |      ||: |     ::|| |::::|:: :|   |   |||:::||
Db         15 FSLATAEQCGQETPLENMLFASFYLLDFILALVGNTLALWLFIRDHKSGTPANVFLMHLA 74

Qy         66 ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMV 125
              ::||   :   ||  |   |:   |::|  ||::|||:   :   |:|||:||||| :|   ||||:|
Db         75 VADLSCVLVLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTCISADRFLAIV 134

Qy        126 HPFRLLHVTSIRSAWILCGIIWILI-MASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQT 184
              || : | :        | : |   :|::: :| : :|:     : |          ||:  ||:   |
Db        135 HPVKSLKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQ--LYR-EKASH 191

Qy        185 MNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHR---KALTTIIITLIIFF 241
                 ::| |     || |    ||||||| |              ||||   |      ||:   |  |  |  ||
Db        192 HALVSLAVAFTFPFITTVTCYLLIIRSL------RQGLRVEKRLKTKAVRMIAIVLAIFL 245

Qy        242 LCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYYFAGENFK 297
              :||:|||   |:|::   ::         |    :      ||      ||     |  :  |     :|::|:|   |  |:
Db        246 VCFVPYHVNRSVYVLHYRSHGASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFR 305

Qy        298 DRLKSAL----RKGHPQKAKTK 315
                |  :  |         ||  |      :  |
Db        306 HALCNLLCGKRLKGPPPSFEGK 327

RESULT 6
US-09-299-843A-44
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; Sequence 44, Application US/09299843A
; Patent No. 6107475
;  GENERAL INFORMATION:
;    APPLICANT:  Godiska, Ronald
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Schweikart, Vicki L.
;    TITLE OF INVENTION:  No. 6107475el Seven Transmembrane Receptors
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/299,843A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/088,337
;      FILING DATE:  01-JUN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/153,848
;      FILING DATE:  17-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/977,452
;      FILING DATE:  17-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jill E. Uhl
;      REGISTRATION NUMBER:  43,213
;      REFERENCE/DOCKET NUMBER:  27866/32059B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  339 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-299-843A-44

  Query Match             28.0%;  Score 479;  DB 3;  Length 339;
  Best Local Similarity   34.8%;  Pred. No. 6.8e-30;
  Matches  112;  Conservative   62;  Mismatches  126;  Indels   22;  Gaps    9;

Qy          7 FSNNNSRNCTIEN-FKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA 65
              ||    :   |   |    :    |    ||: |    ::|| |::::|:: :|   |  |||:::||
Db         15 FSLATAEQCGQETPLENMLFASFYLLDFILALVGNTLALWLFIRDHKSGTPANVFLMHLA 74

Qy         66 ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMV 125
              ::||  :  || |  |:  |::| ||::|||:  :  |:|||:||||| :|  ||||:|
Db         75 VADLSCVLVLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTCISADRFLAIV 134

Qy        126 HPFRLLHVTSIRSAWILCGIIWILI-MASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQT 184
              || : | :     | : |  :|::: :| : :|:   : |         ||:  ||:  |
Db        135 HPVKSLKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQ--LYR-EKASH 191

Qy        185 MNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHR---KALTTIIITLIIFF 241
                 ::| |     || |   ||||||| |          |||| |     ||:  | | | ||
Db        192 HALVSLAVAFTFPFITTVTCYLLIIRSL------RQGLRVEKRLKTKAVRMIAIVLAIFL 245

Qy        242 LCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYYFAGENFK 297
              :||:|||  |:|::  ::       |  :   ||   ||  | : |   :|::|:|  | |:
Db        246 VCFVPYHVNRSVYVLHYRSHGASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFR 305

Qy        298 DRLKSAL----RKGHPQKAKTK 315
                 | : |      || |   : |
Db        306 HALCNLLCGKRLKGPPPSFEGK 327


RESULT 7
US-09-088-337B-44
; Sequence 44, Application US/09088337B
; Patent No. 6348574
;  GENERAL INFORMATION:
;       APPLICANT: Godiska, Ronald
;                  Gray, Patrick W.
;                  Schweikart, Vicki L.
;       TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
;       NUMBER OF SEQUENCES: 66
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
;                       Borun
;            STREET: 6300 Sears Tower, 233 South Wacker Drive
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60606
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/088,337B
;            FILING DATE: 01-Jun-1998
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/153,848
;            FILING DATE: 17-NOV-1993
;            APPLICATION NUMBER: US 07/977,452
;            FILING DATE: 17-NOV-1992
;       ATTORNEY/AGENT INFORMATION:
;            NAME: No. 6348574and, Greta E.
;            REGISTRATION NUMBER: 35,302
;            REFERENCE/DOCKET NUMBER: 31794
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (312) 474-6300
;            TELEFAX: (312) 474-0448
;            TELEX: 25-3856
;  INFORMATION FOR SEQ ID NO: 44:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 339 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-088-337B-44

  Query Match             28.0%;  Score 479;  DB 4;  Length 339;
  Best Local Similarity   34.8%;  Pred. No. 6.8e-30;
  Matches  112;  Conservative   62;  Mismatches  126;  Indels   22;  Gaps    9;

Qy          7 FSNNNSRNCTIEN-FKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA 65
              ||    :   |   |    :    |    ||: |    ::|| |::::|:: :|   |  |||:::||
Db         15 FSLATAEQCGQETPLENMLFASFYLLDFILALVGNTLALWLFIRDHKSGTPANVFLMHLA 74

Qy         66 ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMV 125
              ::||  :  || |  |:  |::| ||::|||:  :  |:|||:||||| :|  ||||:|
Db         75 VADLSCVLVLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTCISADRFLAIV 134

Qy        126 HPFRLLHVTSIRSAWILCGIIWILI-MASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQT 184
              || : | :     | : |  :|::: :| : :|:   : |         ||:  ||:  |
Db        135 HPVKSLKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQ--LYR-EKASH 191

Qy        185 MNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHR---KALTTIIITLIIFF 241
                 ::| |     || |   ||||||| |          |||| |     ||:  | | | ||
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Db        192 HALVSLAVAFTFPFITTVTCYLLIIRSL------RQGLRVEKRLKTKAVRMIAIVLAIFL 245

Qy        242 LCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYYFAGENFK 297
              :||:|||  |:|::  ::      |   :    ||    ||  |  :  |    :|::|:|  | |:
Db        246 VCFVPYHVNRSVYVLHYRSHGASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFR 305

Qy        298 DRLKSAL----RKGHPQKAKTK 315
                 | : |      || |   : |
Db        306 HALCNLLCGKRLKGPPPSFEGK 327
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RESULT 8
US-09-170-496D-32
; Sequence 32, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-32

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  Query Match             28.0%;  Score 479;  DB 4;  Length 339;
  Best Local Similarity   34.8%;  Pred. No. 6.8e-30;
  Matches  112;  Conservative   62;  Mismatches  126;  Indels   22;  Gaps    9;

Qy          7 FSNNNSRNCTIEN-FKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA 65
              ||    :   |   |     :    |     ||: |    ::|| |::::|:: :|   |   |||:::||
Db         15 FSLATAEQCGQETPLENMLFASFYLLDFILALVGNTLALWLFIRDHKSGTPANVFLMHLA 74

Qy         66 ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMV 125
              ::||   :   || |   |:   |::| ||::|||:   :   |:|||:|||||| :|   ||||:|
Db         75 VADLSCVLVLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTCISADRFLAIV 134

Qy        126 HPFRLLHVTSIRSAWILCGIIWILI-MASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQT 184
              || : | :       | : |   :|::: :| : :|:    : |          ||:  ||:   |
Db        135 HPVKSLKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQ--LYR-EKASH 191

Qy        185 MNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHR---KALTTIIITLIIFF 241
                 ::| |      || |     |||||| |                |||  |       ||:  | | | ||
Db        192 HALVSLAVAFTFPFITTVTCYLLIIRSL------RQGLRVEKRLKTKAVRMIAIVLAIFL 245

Qy        242 LCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYYFAGENFK 297
              :||:|||  |:|::  ::      |   :    ||    ||  |  :  |    :|::|:|  | |:
Db        246 VCFVPYHVNRSVYVLHYRSHGASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFR 305

Qy        298 DRLKSAL----RKGHPQKAKTK 315
                 | : |      || |   : |
Db        306 HALCNLLCGKRLKGPPPSFEGK 327
```

RESULT 9
PCT-US93-11153-44
; Sequence 44, Application PC/TUS9311153
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11153
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-11153-44

```
  Query Match             28.0%;  Score 479;  DB 5;  Length 339;
  Best Local Similarity   34.8%;  Pred. No. 6.8e-30;
  Matches  112;  Conservative   62;  Mismatches  126;  Indels   22;  Gaps    9;

Qy          7 FSNNNSRNCTIEN-FKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA 65
              ||    :   |   |     :    |     ||: |    ::|| |::::|:: :|   |   |||:::||
Db         15 FSLATAEQCGQETPLENMLFASFYLLDFILALVGNTLALWLFIRDHKSGTPANVFLMHLA 74

Qy         66 ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMV 125
              ::||   :   || |   |:   |::| ||::|||:   :   |:|||:|||||| :|   ||||:|
Db         75 VADLSCVLVLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTCISADRFLAIV 134

Qy        126 HPFRLLHVTSIRSAWILCGIIWILI-MASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQT 184
              || : | :       | : |   :|::: :| : :|:    : |          ||:  ||:   |
Db        135 HPVKSLKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQ--LYR-EKASH 191

Qy        185 MNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHR---KALTTIIITLIIFF 241
                 ::| |      || |     |||||| |                |||  |       ||:  | | | ||
Db        192 HALVSLAVAFTFPFITTVTCYLLIIRSL------RQGLRVEKRLKTKAVRMIAIVLAIFL 245

Qy        242 LCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYYFAGENFK 297
              :||:|||  |:|::  ::      |   :    ||    ||  |  :  |    :|::|:|  | |:
Db        246 VCFVPYHVNRSVYVLHYRSHGASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFR 305

Qy        298 DRLKSAL----RKGHPQKAKTK 315
                 | : |      || |   : |
Db        306 HALCNLLCGKRLKGPPPSFEGK 327
```

RESULT 10
PCT-US95-07180-2
; Sequence 2, Application PC/TUS9507180
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; APPLICANT: GOCAYNE, JEANINE D
; APPLICANT: RUBEN, STEVEN M
; TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBEB69
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,

```
;       ADDRESSEE:  STEWART & OLSTEIN
;       STREET:  6 BECKER FARM ROAD
;       CITY:  ROSELAND
;       STATE:  NJ
;       COUNTRY:  US
;       ZIP:  07068
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/07180
;       FILING DATE:  06-JUNE-1995
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  MULLINS, J.G.
;       REGISTRATION NUMBER:  30,073
;       REFERENCE/DOCKET NUMBER:  325800-366
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  201-994-1700
;       TELEFAX:  201-994-1744
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  339 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
PCT-US95-07180-2

  Query Match              28.0%;  Score 479;  DB 5;  Length 339;
  Best Local Similarity   34.8%;  Pred. No. 6.8e-30;
  Matches  112;  Conservative   62;  Mismatches  126;  Indels   22;  Gaps    9;

Qy          7 FSNNNSRNCTIEN-FKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA 65
                ||   :  |  |    :   |    ||: |    ::|| |:::|:: :|   |   |||:::||
Db         15 FSLATAEQCGQETPLENMLFASFYLLDFILALVGNTLALWLFIRDHKSGTPANVFLMHLA 74

Qy         66 ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMV 125
              ::||   :   || |   |:   |::|  ||::|||:   :   |:|||:||||| :|   ||||:|
Db         75 VADLSCVLVLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTCISADRFLAIV 134

Qy        126 HPFRLLHVTSIRSAWILCGIIWILI-MASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQT 184
              || : | :         | : |   :|::: :| : :|:    : |         ||:  ||:  |
Db        135 HPVKSLKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQ--LYR-EKASH 191

Qy        185 MNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHR---KALTTIIITLIIFF 241
                 ::| |      || |    |||||| |           ||||   |     ||:   | | | | ||
Db        192 HALVSLAVAFTFPFITTVTCYLLIIRSL------RQGLRVEKRLKTKAVRMIAIVLAIFL 245

Qy        242 LCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYYFAGENFK 297
              :||:|||  |:|::  ::       |  :    ||    ||   | : |      :|::|:|   | |:
Db        246 VCFVPYHVNRSVYVLHYRSHGASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFR 305

Qy        298 DRLKSAL----RKGHPQKAKTK 315
                 | : |       || |    : |
Db        306 HALCNLLCGKRLKGPPPSFEGK 327


RESULT 11
US-09-170-496D-182
; Sequence 182, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/09/170,496D
;  CURRENT FILING DATE:  1998-10-13
;  NUMBER OF SEQ ID NOS: 294
```

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;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 182
;   LENGTH: 339
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-170-496D-182

  Query Match              27.8%;  Score 476;  DB 4;  Length 339;
  Best Local Similarity   34.8%;  Pred. No. 1.2e-29;
  Matches  112;  Conservative   61;  Mismatches  127;  Indels   22;  Gaps    9;

Qy          7 FSNNNSRNCTIEN-FKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA 65
                ||   :  |  |    :   |    ||: |    ::|| |:::|:: :|   |   |||:::||
Db         15 FSLATAEQCGQETPLENMLFASFYLLDFILALVGNTLALWLFIRDHKSGTPANVFLMHLA 74

Qy         66 ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMV 125
              ::||   :   || |   |:   |::|  ||::|||:   :   |:|||:||||| :|   ||||:|
Db         75 VADLSCVLVLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTCISADRFLAIV 134

Qy        126 HPFRLLHVTSIRSAWILCGIIWILI-MASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQT 184
              || : | :         | : |   :|::: :| : :|:    : |         ||:  ||:  |
Db        135 HPVKSLKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQ--LYR-EKASH 191

Qy        185 MNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHR---KALTTIIITLIIFF 241
                 ::| |      || |    |||||| |           ||||   |     ||    | | | | ||
Db        192 HALVSLAVAFTFPFITTVTCYLLIIRSL------RQGLRVEKRLKTKAKRMIAIVLAIFL 245

Qy        242 LCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYYFAGENFK 297
              :||:|||  |:|::  ::       |  :    ||    ||   | : |      :|::|:|   | |:
Db        246 VCFVPYHVNRSVYVLHYRSHGASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFR 305

Qy        298 DRLKSAL----RKGHPQKAKTK 315
                 | : |       || |    : |
Db        306 HALCNLLCGKRLKGPPPSFEGK 327


RESULT 12
US-08-513-974B-374
; Sequence 374, Application US/08513974B
; Patent No. 6114139
;  GENERAL INFORMATION:
;     APPLICANT:  Hinuma, Shuji
;     APPLICANT:  Hosoya, Masaki
;     APPLICANT:  Fujii, Ryo
;     APPLICANT:  Ohtaki, Tetsuya
;     APPLICANT:  Fukusumi, Shoji
;     APPLICANT:  Ohgi, Kazuhiro
;     TITLE OF INVENTION:  G PROTEIN COUPLED RECEPTOR PROTEIN,
;     TITLE OF INVENTION:  PRODUCTION, AND USE THEREOF
;     NUMBER OF SEQUENCES:  380
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;       STREET:  130 Water Street
;       CITY:  Boston
;       STATE:  MA
;       COUNTRY:  USA
;       ZIP:  02109
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/513,974B
;       FILING DATE:  14-SEP-1995
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/JP95/01599
;       FILING DATE:  10-AUG-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 7-093989
;       FILING DATE:  19-AUG-1995
;     PRIOR APPLICATION DATA:
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;       APPLICATION NUMBER:  JP 7-057186
;       FILING DATE:  16-MAR-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 7-007177
;       FILING DATE:  20-JAN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-326611
;       FILING DATE:  28-DEC-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-270017
;       FILING DATE:  02-NOV-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-236357
;       FILING DATE:  30-SEP-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-236356
;       FILING DATE:  30-SEP-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-189274
;       FILING DATE:  11-AUG-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-189273
;       FILING DATE:  11-AUG-1945
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-189272
;       FILING DATE:  11-AUG-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Resnick, David S.
;       REGISTRATION NUMBER:  34,235
;       REFERENCE/DOCKET NUMBER:  45753
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-523-3400
;       TELEFAX:  617-523-6440
;   INFORMATION FOR SEQ ID NO:  374:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  362 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-513-974B-374

  Query Match             26.9%;  Score 461;  DB 3;  Length 362;
  Best Local Similarity   30.7%;  Pred. No. 1.8e-28;
  Matches   98;  Conservative   81;  Mismatches  114;  Indels   26;  Gaps    7;

Qy          5 GTFSNNNSRNCTI--ENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFML 62
                |  : | :  |::     |:  : | ||:::|  | |||  ::|::|:    :   : ::|:|
Db         21 GWAAGNATTKCSLTKTGFQFYYLPTVYILVFITGFLGNSVAIWMFVFHMRPWSGISVYMF 80

Qy         63 NLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFL 122
              |||::| |:: |||      ||     ::|||||: |::   :   :||:| || ||| :|| |:
Db         81 NLALADFLYVLTLPALIFYYFNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISVHRYT 140

Qy        123 AMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLL---DSGSEQNGSVTSCLE------ 173
                :||| : |       ::|  :  ::| |::|     :|      |  :| ::| | :
Db        141 GVVHPLKSLGRLKKKNAVYVSSLVWALVVAVIAPILFYSGIGVRRNKTIT-CYDTTADEY 199

Qy        174 LNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTI 233
               |  | :  : |   :: :         ||   :   || ||:: |:  ::   | ||     ||:    :
Db        200 LRSYFVYSMCTTVFMFCI-----PFIVILGCYGLIVKALIYKDLDNSPLR---RKSTYLV 251

Qy        234 IITLIIFFLCFLPYHTLRTVHL------TTWKVGLCKDRLHKALVITLALAAANACFNPL 287
              || | :| : :||:| ::|::|           | ::      |:::     :|   ||: |:| :|:
Db        252 IIVLTVFAVSYLPFHVMKTLNLRARLDFQTPQMCAFNDKVYATYQVTRGLASLNSCVDPI 311

Qy        288 LYYFAGENFKDRLKSALRK 306
              ||: ||: |: ||   | ||
Db        312 LYFLAGDTFRRRLSRATRK 330


RESULT 13
US-08-559-524A-4
; Sequence 4, Application US/08559524A
; Patent No. 5871963
;  GENERAL INFORMATION:
;    APPLICANT:  Conley, Pamela B.
;    APPLICANT:  Jantzen, Hans-Michael
;    TITLE OF INVENTION:  NOVEL PURINERGIC RECEPTOR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN, LEWIS & BOCKIUS LLP
;      STREET:  1800 M Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20036-5869
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/559,524A
;      FILING DATE:  15-NOV-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Adler, Reid G.
;      REGISTRATION NUMBER:  30,988
;      REFERENCE/DOCKET NUMBER:  044481-5010-00-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-467-7000
;      TELEFAX:  202-467-7176
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  373 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-559-524A-4

  Query Match             25.8%;  Score 442;  DB 2;  Length 373;
  Best Local Similarity   31.0%;  Pred. No. 5.4e-27;
  Matches   95;  Conservative   78;  Mismatches  109;  Indels   24;  Gaps    7;

Qy         16 TIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLLFISTL 75
                |   |:  :  |  ||:::|   | |||  ::|::|:    |    :  ::|:|  |||::|  |:: ||
Db         45 TKTGFQFYYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTL 104

Qy         76 PFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPFRLLHVTS 135
                |      ||    ::|||||   |::   :    :||:| || ||| :|   |:    :|:| :  |
Db        105 PALIFYYFNKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLK 164

Qy        136 IRSAWILCGIIWILIMASSIMLL---DSGSEQNGSVTSCLE------LNLYKIAKLQTMN 186
                ::|   :   ::|::::          :|        :|    :|  ::| | :           |   |  |    :  |
Db        165 KKNAVYISVLVWLIVVVGISPILFYSGTGIRKNKTIT-CYDTTSDEYLRSYFIYSMCT-- 221

Qy        187 YIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFLP 246
                  :  :  |  :|      :   || ||:| |:   ::     |  ||       ||::   :|| |  :|  :  ::|
Db        222 --TVAMFC-VPLVLILGCYGLIVRALIYKDLDNSPLR---RKSIYLVTIVLTVFAVSYIP 275

Qy        247 YHTLRTVHL------TTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
              :|  ::|::|               | ::          ||::       :|    ||:  |:|  :|:||:  ||:  |:  ||
Db        276 FHVMKTMNLRARLDFQTPEMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335

Qy        301 KSALRK 306
                 |  ||
Db        336 SRATRK 341


RESULT 14
US-08-749-707-4
; Sequence 4, Application US/08749707
; Patent No. 6063582
;  GENERAL INFORMATION:
```

```
;     APPLICANT:  Conley, Pamela B.
;     APPLICANT:  Jantzen, Hans-Michael
;     TITLE OF INVENTION:  NOVEL PURINERGIC RECEPTOR
;     NUMBER OF SEQUENCES:  14
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  MORGAN, LEWIS & BOCKIUS LLP
;       STREET:  1800 M Street, N.W.
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  USA
;       ZIP:  20036-5869
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/749,707
;       FILING DATE:  15-NOV-1996
;       CLASSIFICATION:  536
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Adler, Reid G.
;       REGISTRATION NUMBER:  30,988
;       REFERENCE/DOCKET NUMBER:  044481-5010-01-US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-467-7000
;       TELEFAX:  202-467-7176
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  373 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-749-707-4

  Query Match             25.8%;  Score 442;  DB 3;  Length 373;
  Best Local Similarity   31.0%;  Pred. No. 5.4e-27;
  Matches   95;  Conservative   78;  Mismatches  109;  Indels   24;  Gaps    7;

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Db        165 KKNAVYISVLVWLIVVVGISPILFYSGTGIRKNKTIT-CYDTTSDEYLRSYFIYSMCT-- 221

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Qy        301 KSALRK 306
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Db        336 SRATRK 341
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RESULT 15
US-08-383-750-4
; Sequence 4, Application US/08383750
; Patent No. 5744301
;  GENERAL INFORMATION:
;    APPLICANT:  Birkenbach, Mark
;    APPLICANT:  Kieff, Elliot
;    TITLE OF INVENTION:  Epstein Barr Virus Induced Genes
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue, N.W.,
;      STREET:  Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/383,750
;      FILING DATE:  Herewith
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fox, Samuel, L.
;      REGISTRATION NUMBER:  30,353
;      REFERENCE/DOCKET NUMBER:  0627.3300001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  361 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-383-750-4

  Query Match             25.7%;  Score 440;  DB 1;  Length 361;
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Qy        181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVE-----VPESGLRVSHRKALTTIII 235
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Qy        236 TLIIFFLCFLPYHTLRTVHLTTWKVGL-----CKDR--LHKALVITLALAAANACFNPLL 288
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Search completed: October  8, 2003, 08:27:28
Job time : 22 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 8, 2003, 08:27:32 ; Search time 30 Seconds
(without alignments)
1772.413 Million cell updates/sec

Title: US-09-991-225-2
Perfect score: 1712
Sequence: 1 MEPNGTFSNNNSRNCTIENF.....KAKTKCVFPVSVWLRKETRV 330

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1712	100.0	330	12	US-09-991-225-2	Sequence 2, Appli
3	1712	100.0	342	12	US-09-991-225-55	Sequence 55, Appl
4	1712	100.0	346	9	US-09-826-791-6	Sequence 6, Appli
5	1712	100.0	346	10	US-09-866-230-7	Sequence 7, Appli
6	1712	100.0	346	10	US-09-866-230-9	Sequence 9, Appli
7	1712	100.0	346	10	US-09-828-478-2	Sequence 2, Appli
8	1712	100.0	346	11	US-09-779-679-2	Sequence 2, Appli
9	1712	100.0	346	11	US-09-779-679-26	Sequence 26, Appl
10	1712	100.0	346	12	US-09-991-225-30	Sequence 30, Appl
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12	1712	100.0	346	12	US-10-321-807-14	Sequence 14, Appl
13	1712	100.0	346	15	US-10-225-567A-589	Sequence 589, App
14	1706	99.6	346	12	US-10-321-807-88	Sequence 88, Appl
15	564	32.9	337	15	US-10-290-078-21	Sequence 21, Appl
16	559	32.7	337	10	US-09-866-230-8	Sequence 8, Appli
17	559	32.7	337	10	US-09-828-478-5	Sequence 5, Appli
18	559	32.7	337	11	US-09-779-679-27	Sequence 27, Appl
19	559	32.7	337	12	US-09-991-225-6	Sequence 6, Appli
20	559	32.7	337	12	US-10-349-021-5	Sequence 5, Appli
21	559	32.7	337	15	US-10-225-567A-547	Sequence 547, App
22	557	32.5	337	15	US-10-167-192-3	Sequence 3, Appli
23	487.5	28.5	337	9	US-09-943-798-4	Sequence 4, Appli
24	487.5	28.5	337	11	US-09-885-453-1	Sequence 1, Appli
25	487.5	28.5	337	12	US-10-017-161-526	Sequence 526, App
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27	487.5	28.5	337	12	US-10-010-568-2	Sequence 2, Appli
28	487.5	28.5	337	12	US-10-321-807-28	Sequence 28, Appl
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30	487.5	28.5	337	15	US-10-270-144-2	Sequence 2, Appli
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32	487.5	28.5	337	15	US-10-076-384-14	Sequence 14, Appl
33	485.5	28.4	337	15	US-10-225-567A-647	Sequence 647, App
34	479	28.0	339	9	US-09-848-889-12	Sequence 12, Appl
35	479	28.0	339	9	US-09-798-133-2	Sequence 2, Appli
36	479	28.0	339	10	US-09-828-478-4	Sequence 4, Appli
37	479	28.0	339	12	US-09-991-225-8	Sequence 8, Appli
38	479	28.0	339	12	US-10-349-021-4	Sequence 4, Appli
39	479	28.0	339	12	US-10-100-982-12	Sequence 12, Appl
40	479	28.0	339	12	US-10-268-332-14	Sequence 14, Appl
41	479	28.0	339	12	US-09-964-821B-14	Sequence 14, Appl
42	479	28.0	339	15	US-10-251-385-32	Sequence 32, Appl
43	479	28.0	367	10	US-09-828-478-6	Sequence 6, Appli
44	479	28.0	367	12	US-10-349-021-6	Sequence 6, Appli
45	479	28.0	367	15	US-10-225-567A-304	Sequence 304, App

ALIGNMENTS

RESULT 1
US-09-826-791-2
; Sequence 2, Application US/09826791
; Patent No. US20010039037A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc
; TITLE OF INVENTION: No. US20010039037A1e1 Polypeptide
; FILE REFERENCE: PC10914ADAM
; CURRENT APPLICATION NUMBER: US/09/826,791
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 0008504.3
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/198,367
; PRIOR FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-791-2

Query Match 100.0%; Score 1712; DB 9; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.1e-140;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 FLAVVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLDSGSEQNGSVTSCLELNLYKIA 180
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RESULT 2
US-09-991-225-2
; Sequence 2, Application US/09991225
; Publication No. US20030153063A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, EXPRESSED HI
;  TITLE OF INVENTION:  HEART AND VARIANTS THEREOF
;  FILE REFERENCE: D0075.NP
;  CURRENT APPLICATION NUMBER: US/09/991,225
;  CURRENT FILING DATE:  2001-11-16
;  PRIOR APPLICATION NUMBER: 60/249,613
;  PRIOR FILING DATE: 2000-11-17
;  PRIOR APPLICATION NUMBER: 60/257,611
;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: 60/305,818
;  PRIOR FILING DATE: 2001-07-16
;  NUMBER OF SEQ ID NOS: 81
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 330
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-09-991-225-2

  Query Match             100.0%;  Score 1712;  DB 12;  Length 330;
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  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 3
US-09-991-225-55
; Sequence 55, Application US/09991225
; Publication No. US20030153063A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, EXPRESSE
;  TITLE OF INVENTION:  HEART AND VARIANTS THEREOF
;  FILE REFERENCE: D0075.NP
;  CURRENT APPLICATION NUMBER: US/09/991,225
;  CURRENT FILING DATE:  2001-11-16
;  PRIOR APPLICATION NUMBER: 60/249,613
;  PRIOR FILING DATE: 2000-11-17
;  PRIOR APPLICATION NUMBER: 60/257,611
;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: 60/305,818
;  PRIOR FILING DATE: 2001-07-16
;  NUMBER OF SEQ ID NOS: 81
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
;   LENGTH: 341
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-991-225-55

  Query Match             100.0%;  Score 1712;  DB 12;  Length 341;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-140;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 4
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; Sequence 6, Application US/09826791
; Patent No. US20010039037A1
; GENERAL INFORMATION:
;  APPLICANT: Pfizer Inc
;  TITLE OF INVENTION: No. US20010039037A1el Polypeptide
;  FILE REFERENCE: PC10914ADAM
;  CURRENT APPLICATION NUMBER: US/09/826,791
;  CURRENT FILING DATE:  2001-04-05
;  PRIOR APPLICATION NUMBER: 0008504.3
;  PRIOR FILING DATE: 2000-04-05
;  PRIOR APPLICATION NUMBER: 60/198,367
;  PRIOR FILING DATE: 2000-04-19
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-826-791-6

  Query Match             100.0%;  Score 1712;  DB 9;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-140;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Db         77 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 136

Qy        121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 196

Qy        181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
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Qy        301 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
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Db        317 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 346


RESULT 5
US-09-866-230-7
; Sequence 7, Application US/09866230
; Patent No. US20020150901A1
; GENERAL INFORMATION:
;  APPLICANT: Murphy, Andrew, et al.
;  TITLE OF INVENTION: No. US20020150901A1el Nucleic Acids, Polypeptides, Methods of Mak
;  FILE REFERENCE: REG 771A
;  CURRENT APPLICATION NUMBER: US/09/866,230
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: 60/207,725
;  PRIOR FILING DATE: 2000-05-26
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.0
;  SEQ ID NO 7
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-866-230-7

  Query Match          100.0%;  Score 1712;  DB 10;  Length 346;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-140;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFPPIVYLIIFPWGVLGNGLSIYVFLQPYKKSTSVNVF 60
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Db         17 MEPNGTFSNNNSRNCTIENFKREFPPIVYLIIFPWGVLGNGLSIYVFLQPYKKSTSVNVF 76

Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 136

Qy        121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 196

Qy        181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
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Db        197 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 256

Qy        241 FLCFLPYHTLRTVHLTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
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Db        257 FLCFLPYHTLRTVHLTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 316

Qy        301 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
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Db        317 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 346


RESULT 6
US-09-866-230-9
; Sequence 9, Application US/09866230
; Patent No. US20020150901A1
; GENERAL INFORMATION:
;  APPLICANT: Murphy, Andrew, et al.
;  TITLE OF INVENTION: No. US20020150901A1el Nucleic Acids, Polypeptides, Methods of
;  FILE REFERENCE: REG 771A
;  CURRENT APPLICATION NUMBER: US/09/866,230
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: 60/207,725
;  PRIOR FILING DATE: 2000-05-26
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.0
;  SEQ ID NO 9
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-866-230-9

  Query Match          100.0%;  Score 1712;  DB 10;  Length 346;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-140;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFPPIVYLIIFPWGVLGNGLSIYVFLQPYKKSTSVNVF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 MEPNGTFSNNNSRNCTIENFKREFPPIVYLIIFPWGVLGNGLSIYVFLQPYKKSTSVNVF 76

Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
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Db         77 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 136

Qy        121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
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Db        137 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 196

Qy        181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 256

Qy        241 FLCFLPYHTLRTVHLTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
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Db        257 FLCFLPYHTLRTVHLTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 316

Qy        301 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
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Db        317 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 346


RESULT 7
US-09-828-478-2
; Sequence 2, Application US/09828478
; Patent No. US20020155528A1
; GENERAL INFORMATION:
;  APPLICANT: Xiao, Yonghong
;  TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
;  TITLE OF INVENTION: Protein
;  FILE REFERENCE: 04974.00458
;  CURRENT APPLICATION NUMBER: US/09/828,478
;  CURRENT FILING DATE:  2001-04-09
;  PRIOR APPLICATION NUMBER: 60/195,196
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: 60/254,876
;  PRIOR FILING DATE: 2000-12-13
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-828-478-2
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  Query Match           100.0%;  Score 1712;  DB 10;  Length 346;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-140;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLLIFFWGVLGNGLSIVVFLQPYKKSTSVNVF 60
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Db         17 MEPNGTFSNNNSRNCTIENFKREFFPIVYLLIFFWGVLGNGLSIVVFLQPYKKSTSVNVF 76

Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 136

Qy        121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSRQNGSVTSCLELNLYKIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSRQNGSVTSCLELNLYKIA 196

Qy        181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 256

Qy        241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 316

Qy        301 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
              ||||||||||||||||||||||||||||||
Db        317 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 346


RESULT 8
US-09-779-679-2
; Sequence 2, Application US/09779679
; Publication No. US20030082757A1
; GENERAL INFORMATION:
;  APPLICANT:  Taupier, Raymond J
;  APPLICANT:  Burgess, Catherine E
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Mishra, Vishnu S
;  APPLICANT:  Casman, Stacie
;  APPLICANT:  Ballinger, Robert
;  APPLICANT:  Vernet, Corine A
;  APPLICANT:  Li, Li
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Andrew, David P
;  APPLICANT:  Mezes, Peter S
;  TITLE OF INVENTION: No. US20030082757A1el Proteins and Nucleic Acids Encoding the Sam
;  FILE REFERENCE: 15966-661
;  CURRENT APPLICATION NUMBER: US/09/779,679
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: USSN 60/181045
;  PRIOR FILING DATE:  2000-02-08
;  PRIOR APPLICATION NUMBER: USSN 60/183191
;  PRIOR FILING DATE:  2000-02-17
;  PRIOR APPLICATION NUMBER: USSN 60/180,929
;  PRIOR FILING DATE:  2000-02-08
;  PRIOR APPLICATION NUMBER: USSN 60/219758
;  PRIOR FILING DATE:  2000-07-20
;  PRIOR APPLICATION NUMBER: USSN 60/181339
;  PRIOR FILING DATE:  2000-02-09
;  PRIOR APPLICATION NUMBER: USSN 60/181344
;  PRIOR FILING DATE:  2000-02-09
;  PRIOR APPLICATION NUMBER: USSN 60/221341
;  PRIOR FILING DATE:  2000-07-26
;  PRIOR APPLICATION NUMBER: USSN 60/181392
;  PRIOR FILING DATE:  2000-02-09
;  PRIOR APPLICATION NUMBER: USSN 60/219585
;  PRIOR FILING DATE:  2000-07-20
;  PRIOR APPLICATION NUMBER: USSN 60/181157
;  PRIOR FILING DATE:  2000-02-09
;  NUMBER OF SEQ ID NOS:  65
;  SOFTWARE:  PatentIn Ver. 2.0

; SEQ ID NO 2
;  LENGTH:  346
;  TYPE:  PRT
;  ORGANISM:  Homo sapiens
US-09-779-679-2

  Query Match           100.0%;  Score 1712;  DB 11;  Length 346;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-140;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLLIFFWGVLGNGLSIVVFLQPYKKSTSVNVF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 MEPNGTFSNNNSRNCTIENFKREFFPIVYLLIFFWGVLGNGLSIVVFLQPYKKSTSVNVF 76

Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 136

Qy        121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSRQNGSVTSCLELNLYKIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSRQNGSVTSCLELNLYKIA 196

Qy        181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 256

Qy        241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 316

Qy        301 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
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Db        317 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 346


RESULT 9
US-09-779-679-26
; Sequence 26, Application US/09779679
; Publication No. US20030082757A1
; GENERAL INFORMATION:
;  APPLICANT:  Taupier, Raymond J
;  APPLICANT:  Burgess, Catherine E
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Mishra, Vishnu S
;  APPLICANT:  Casman, Stacie
;  APPLICANT:  Ballinger, Robert
;  APPLICANT:  Vernet, Corine A
;  APPLICANT:  Li, Li
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Andrew, David P
;  APPLICANT:  Mezes, Peter S
;  TITLE OF INVENTION: No. US20030082757A1el Proteins and Nucleic Acids Encoding the
;  FILE REFERENCE: 15966-661
;  CURRENT APPLICATION NUMBER: US/09/779,679
;  CURRENT FILING DATE:  2001-02-08
;  PRIOR APPLICATION NUMBER: USSN 60/181045
;  PRIOR FILING DATE:  2000-02-08
;  PRIOR APPLICATION NUMBER: USSN 60/183191
;  PRIOR FILING DATE:  2000-02-17
;  PRIOR APPLICATION NUMBER: USSN 60/180,929
;  PRIOR FILING DATE:  2000-02-08
;  PRIOR APPLICATION NUMBER: USSN 60/219758
;  PRIOR FILING DATE:  2000-07-20
;  PRIOR APPLICATION NUMBER: USSN 60/181339
;  PRIOR FILING DATE:  2000-02-09
;  PRIOR APPLICATION NUMBER: USSN 60/181344
;  PRIOR FILING DATE:  2000-02-09
;  PRIOR APPLICATION NUMBER: USSN 60/221341
;  PRIOR FILING DATE:  2000-07-26
;  PRIOR APPLICATION NUMBER: USSN 60/181392
;  PRIOR FILING DATE:  2000-02-09
;  PRIOR APPLICATION NUMBER: USSN 60/219585
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;  PRIOR FILING DATE: 2000-07-20
;  PRIOR APPLICATION NUMBER: USSN 60/181157
;  PRIOR FILING DATE: 2000-02-09
;  NUMBER OF SEQ ID NOS: 65
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
;    LENGTH: 346
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-779-679-26

  Query Match           100.0%;  Score 1712;  DB 11;  Length 346;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-140;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFPPIVYLIIFWGVLGNGLSIYVFLQPYKKSTSVNVF 60
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Db         17 MEPNGTFSNNNSRNCTIENFKREFPPIVYLIIFWGVLGNGLSIYVFLQPYKKSTSVNVF 76

Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 136

Qy        121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 196

Qy        181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLTIF 240
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Db        197 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLTIF 256

Qy        241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 316

Qy        301 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
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Db        317 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 346


RESULT 10
US-09-991-225-30
; Sequence 30, Application US/09991225
; Publication No. US20030153063A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, EXPRESSED HI
; TITLE OF INVENTION: HEART AND VARIANTS THEREOF
;  FILE REFERENCE: D0075.NP
;  CURRENT APPLICATION NUMBER: US/09/991,225
;  CURRENT FILING DATE:  2001-11-16
;  PRIOR APPLICATION NUMBER: 60/249,613
;  PRIOR FILING DATE: 2000-11-17
;  PRIOR APPLICATION NUMBER: 60/257,611
;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: 60/305,818
;  PRIOR FILING DATE: 2001-07-16
;  NUMBER OF SEQ ID NOS: 81
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
;    LENGTH: 346
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-991-225-30

  Query Match           100.0%;  Score 1712;  DB 12;  Length 346;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-140;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFPPIVYLIIFWGVLGNGLSIYVFLQPYKKSTSVNVF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 MEPNGTFSNNNSRNCTIENFKREFPPIVYLIIFWGVLGNGLSIYVFLQPYKKSTSVNVF 76

Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 136

Qy        121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 196

Qy        181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLTIF 240
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Db        197 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLTIF 256

Qy        241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
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Db        257 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 316

Qy        301 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
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Db        317 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 346


RESULT 11
US-10-349-021-2
; Sequence 2, Application US/10349021
; Publication No. US20030157541A1
; GENERAL INFORMATION:
;  APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
; TITLE OF INVENTION:  Protein
; FILE REFERENCE: 04974.00458
; CURRENT APPLICATION NUMBER: US/10/349,021
; CURRENT FILING DATE:  2003-01-23
; PRIOR APPLICATION NUMBER: US/09/828,478
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,196
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/254,876
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;    LENGTH: 346
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-349-021-2

  Query Match           100.0%;  Score 1712;  DB 12;  Length 346;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-140;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFPPIVYLIIFWGVLGNGLSIYVFLQPYKKSTSVNVF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 MEPNGTFSNNNSRNCTIENFKREFPPIVYLIIFWGVLGNGLSIYVFLQPYKKSTSVNVF 76

Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 136

Qy        121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
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Db        137 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 196

Qy        181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLTIF 240
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Db        197 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLTIF 256

Qy        241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 316

Qy        301 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
              ||||||||||||||||||||||||||||||
Db        317 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 346
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RESULT 12
US-10-321-807-14
; Sequence 14, Application US/10321807
; Publication No. US20030166148A1
; GENERAL INFORMATION:
;  APPLICANT: Chen, Rupong
;  APPLICANT:  Dang, Huong T.
;  APPLICANT:  Lowitz, Kevin P.
;  TITLE OF INVENTION: No. US20030166148A1-Endogenous, Constitutively Activated Human G
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: ARNO086
;  CURRENT APPLICATION NUMBER: US/10/321,807
;  CURRENT FILING DATE:  2002-12-16
;  PRIOR APPLICATION NUMBER: US/09/714,008
;  PRIOR FILING DATE: 2000-11-16
;  PRIOR APPLICATION NUMBER: 09/170,496
;  PRIOR FILING DATE: 1999-11-17
;  PRIOR APPLICATION NUMBER: PCT/US99/23938
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: 60/166,088
;  PRIOR FILING DATE: 1999-11-17
;  PRIOR APPLICATION NUMBER: 60/166,099
;  PRIOR FILING DATE: 1999-11-17
;  PRIOR APPLICATION NUMBER: 60/166,369
;  PRIOR FILING DATE: 1999-11-17
;  PRIOR APPLICATION NUMBER: 60/171,902
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/171,901
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/171,900
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/181,749
;  PRIOR FILING DATE: 2000-02-11
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
;  LENGTH: 346
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-321-807-14

  Query Match             100.0%;  Score 1712;  DB 12;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-140;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 60
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Db         17 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 76

Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIPGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
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Db         77 MLNLAISDLLFISTLPFRADYYLRGSNWIPGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 136

Qy        121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
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Db        197 KLQTMMYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPEGLRVSHRKALTTIIITLIIF 256

Qy        241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
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Db        257 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 316

Qy        301 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
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RESULT 13
US-10-225-567A-589
; Sequence 589, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
;  APPLICANT: LifeSpan Biosciences
;  APPLICANT:  Brown, Joseph P.
;  APPLICANT:  Burmer, Glenna C.
;  APPLICANT:  Roush, Christine L.
;  TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEP
;  FILE REFERENCE: 1920-4-4
;  CURRENT APPLICATION NUMBER: US/10/225,567A
;  CURRENT FILING DATE:  2001-12-19
;  PRIOR APPLICATION NUMBER: 60/257,144
;  PRIOR FILING DATE: 2000-12-19
;  NUMBER OF SEQ ID NOS: 2292
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 589
;  LENGTH: 346
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-225-567A-589

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  Best Local Similarity   100.0%;  Pred. No. 1.2e-140;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 60
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Db         17 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 76

Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIPGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
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Db         77 MLNLAISDLLFISTLPFRADYYLRGSNWIPGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 136

Qy        121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
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Db        137 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 196

Qy        181 KLQTMMYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPEGLRVSHRKALTTIIITLIIF 240
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Qy        241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
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RESULT 14
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; Sequence 88, Application US/10321807
; Publication No. US20030166148A1
; GENERAL INFORMATION:
;  APPLICANT: Chen, Rupong
;  APPLICANT:  Dang, Huong T.
;  APPLICANT:  Lowitz, Kevin P.
;  TITLE OF INVENTION: No. US20030166148A1-Endogenous, Constitutively Activated Human
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: ARNO086
;  CURRENT APPLICATION NUMBER: US/10/321,807
;  CURRENT FILING DATE:  2002-12-16
;  PRIOR APPLICATION NUMBER: US/09/714,008
;  PRIOR FILING DATE: 2000-11-16
;  PRIOR APPLICATION NUMBER: 09/170,496
;  PRIOR FILING DATE: 1999-11-17
;  PRIOR APPLICATION NUMBER: PCT/US99/23938
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: 60/166,088
;  PRIOR FILING DATE: 1999-11-17
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;  PRIOR APPLICATION NUMBER: 60/166,099
;  PRIOR FILING DATE: 1999-11-17
;  PRIOR APPLICATION NUMBER: 60/166,369
;  PRIOR FILING DATE: 1999-11-17
;  PRIOR APPLICATION NUMBER: 60/171,902
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/171,901
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/171,900
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/181,749
;  PRIOR FILING DATE: 2000-02-11
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 88
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-321-807-88

  Query Match             99.6%;  Score 1706;  DB 12;  Length 346;
  Best Local Similarity   99.7%;  Pred. No. 3.8e-140;
  Matches  329;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
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Qy        181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIF 240
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Qy        241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
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RESULT 15
US-10-290-078-21
; Sequence 21, Application US/10290078
; Publication No. US20030124596A1
; GENERAL INFORMATION:
;  APPLICANT: Carroll, Joseph A.
;  TITLE OF INVENTION: Methods and Compositions for Treating
;  TITLE OF INVENTION:  Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
;  TITLE OF INVENTION:  14395, 14618, 17692 or 58874
;  FILE REFERENCE: MPI2001-288P1(M)
;  CURRENT APPLICATION NUMBER: US/10/290,078
;  CURRENT FILING DATE:  2002-11-07
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
;   LENGTH: 337
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-290-078-21

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Qy         11 NSRNC--TIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISD 68
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Db         10 SSATCHDTIDDFRNQVYSTLYSMISVVGFFGNGFVLYVLIKTYHKKSAFQVYMINLAVAD 69

Qy         69 LLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPF 128
              || : ||| |  ||:    |:|||  ||: :|:|||:| ||:|:| :|  | :|:| |
Db         70 LLCVCTLPLRVVYYVHKGIWLFGDFLCRLSTYALYVNLYCSIFFMTAMSFFRCIAIVFPV 129

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              : ::: : : |  :|  ||| :|: || |:    :   : | | |        |  :  :
Db        130 QNINLVTQKKARFVCVGIWIFVILTSSPFLMAKPQKDEKNNTKCFEPPQDNQTKNHVLVL 189

Qy        186 NYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFL 245
              :|::|||| ::||   : :|| :||  |||  : ::     ||:||:  |::     | : |:
Db        190 HYVSLVVGFIIPFVIIIVCYTMIILTLLKKSMKKN--LSSHKKAIGMIMVVTAAFLVSFM 247

Qy        246 PYHTLRTVHLTTW--KVGLCKD--RLHKALVITLALAAANACFNPLLYYFAGENFKDRLK 301
              |||  ||:||      :     |     |: |::||||:|||:| ||:||||:|:| ||: ||
Db        248 PYHIQRTIHLHFLHNETKPCDSVLRMQKSVVITLSLAASNCCFDPLLYFFSGGNFRKRL- 306

Qy        302 SALRK 306
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Db        307 STFRK 311


Search completed: October  8, 2003, 08:32:40
Job time : 32 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 8, 2003, 08:26:59 ; Search time 85 Seconds
(without alignments)
616.233 Million cell updates/sec

Title: US-09-991-225-2
Perfect score: 1712
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1712	100.0	330	23	AAG77964	Human G-protein co
2	1712	100.0	330	24	ABU11900	Human G-protein co
3	1712	100.0	341	22	AAD07539	Human G-protein co
4	1712	100.0	341	24	ABU11939	Human G-protein co
5	1712	100.0	346	22	AAE12032	Human G-protein co
6	1712	100.0	346	22	AAB82852	Human P2Y-like GPC
7	1712	100.0	346	22	AAE07538	Human G-protein co
8	1712	100.0	346	22	AAU04368	Human G-protein co
9	1712	100.0	346	22	AAU07294	Cysteinyl leukotri
10	1712	100.0	346	22	AAB73097	Human L7C4 recepto
11	1712	100.0	346	23	ABP95624	Human GPCR polypep
12	1712	100.0	346	23	ABU66684	Human novel polype
13	1712	100.0	346	23	AAU10004	Human CysLT2-like
14	1712	100.0	346	23	AAB17231	Human CysLT2 GPCR
15	1712	100.0	346	23	AAG77965	Human G-protein co
16	1712	100.0	346	23	ABB05229	Human LTD4-like G
17	1712	100.0	346	24	ABP81707	Human cysteinyl le
18	1712	100.0	346	24	ABU11923	Human G-protein co
19	1706	99.6	346	22	AAN04393	Human G-protein co
20	1703	99.5	346	22	AAE08553	Human G-protein co
21	1673.5	97.8	331	22	AAB85097	Truncated cysLT2 c
22	1673.5	97.8	347	22	AAB85094	Human cysLT2 cyste
23	1590	92.9	308	24	ABU11962	Human HGPRBMY11 N-
24	1516	88.6	293	24	ABU11963	Human HGPRBMY11 C-
25	1367.5	79.9	345	22	AAB73098	Pig LTC4 receptor
26	1187	69.3	309	22	AAB85095	Rat cysLT-like rec
27	1187	69.3	309	22	AAB73099	Rat LTC4 receptor
28	612	35.7	126	22	AAM25841	Human protein sequ
29	559	32.7	337	19	AAW85047	A human 7-transmem
30	559	32.7	337	19	AAW75799	Human 7-transmembr
31	559	32.7	337	22	AAB85096	Human cysLT-like r
32	559	32.7	337	22	AAE02492	Human CON166 G pro
33	559	32.7	337	24	ABP81686	Human cysteinyl le
34	559	32.7	337	24	ABU11904	Human cysteinyl le
35	557	32.5	337	21	AAY79563	Human G protein co
36	487.5	28.5	337	22	AAU04375	Human G-protein co
37	487.5	28.5	337	23	ABP95602	Human GPCR polypep
38	487.5	28.5	337	23	ABG70271	Human Purinoceptor
39	487.5	28.5	337	23	ABG76871	Human G-protein co
40	487.5	28.5	337	23	ABD70287	Human novel polype
41	487.5	28.5	337	23	AAO15399	Human G protein-co
42	487.5	28.5	337	23	ABB81902	Human G-protein co
43	487.5	28.5	337	23	ABB83819	Human P2Y-like rec
44	487.5	28.5	337	23	AAE22803	Human AXOR89 (G-pr
45	487.5	28.5	337	23	ABB79438	Human P2Y1-li. Ho

ALIGNMENTS

RESULT 1
AAG77964
ID AAG77964 standard; Protein; 330 AA.
XX
AC AAG77964;
XX
DT 25-FEB-2002 (first entry)
XX
DE Human G-protein coupled receptor PFI-017.
XX
KW Human; G-protein coupled receptor; GPCR; PFI-017; cytostatic; neoplastic;
KW antiallergic; osteopathic; cardiovascular; immunosuppressive;
KW gene therapy; heart disease; gastrointestinal disease; sleep disorder;
KW immunological disorder; pulmonary disorder; infectious disease;
KW myeloproliferative disease; allergic rhinitis; asthma; COPD; obesity;
KW chronic obstructive pulmonary disease; inflammatory bowel disease;
KW diabetes; metabolic disease; neurological disease; urogenital disease;
KW inflammation; cancer; osteoporosis; cardiovascular disease; infection;
KW allergy; respiratory disease; sensory organ disorder; hair loss;
KW immunological disorder; pulmonary disease; neoplastic disease;
KW vasculitic granulomatous disease; dermatology; psychotherapeutic.
XX
OS Homo sapiens.
XX
PN US2001039037-A1.
XX
PD 08-NOV-2001.
XX
PF 05-APR-2001; 2001US-0826791.
XX
PR 05-APR-2000; 2000GB-0008504.
PR 19-APR-2000; 2000US-198367P.

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XX
PA   (HARL/) HARLAND L.
XX
PI   Harland L;
XX
DR   WPI; 2002-040722/05.
DR   N-PSDB; AAH77276.
XX
PT   New PFI-017 protein and polynucleotide encoding the protein, useful for
PT   diagnosing or treating metabolic diseases, urogenital disease,
PT   immunological disorders, infectious diseases, neoplastic or
PT   myeloproliferative diseases -
XX
PS   Claim 7; Fig 6B; 39pp; English.
XX
CC   The sequence represents a novel G-protein coupled receptor (GPCR),
CC   PFI-017 of the invention. The PFI-017 has cytostatic, antiallergic,
CC   osteopathic, cardiovascular, and immunosuppressive activity. The
CC   polynucleotides may have a use in gene therapy. The polynucleotide is
CC   useful for treating allergic disorders, an inflammatory disorder, an
CC   immunological disorder, a pulmonary disorder, an infectious disease, a
CC   neoplastic or myeloproliferative disease, or a heart disease. The
CC   allergic disorder is an allergic rhinitis or asthma, the pulmonary
CC   disease is COPD, and the inflammatory disorder is inflammatory bowel
CC   disease. PFI-017 polynucleotide sequences may be used for the diagnosis
CC   of diseases resulting from expression of PFI-017, and to detect and
CC   quantify gene expression in conditions, disorders or diseases in which
CC   PFI-017 activity may be implicated. The polypeptides are used to produce
CC   anti-PFI-017 antibodies to be used diagnostically to detect and quantify
CC   PFI-017 levels in disease states. The antibodies, compounds and
CC   compositions which can modulate the peptide can be used in treating
CC   obesity, diabetes and metabolic disease, neurological disease, urogenital
CC   disease, inflammation, cancer, osteoporosis, cardiovascular disease,
CC   gastrointestinal disease, infections, allergy and respiratory disease,
CC   sensory organ disorders, sleep disorders, hair loss, immunological
CC   disorders, pulmonary diseases, infectious diseases, neoplastic and
CC   myeloproliferative diseases, vasculitic granulomatous diseases, and heart
CC   diseases. These may also be used in dermatology, and psychotherapeutics.
XX
SQ   Sequence   330 AA;

     Query Match             100.0%;  Score 1712;  DB 23;  Length 330;
     Best Local Similarity   100.0%;  Pred. No. 5.4e-177;
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Qy           1 MEPNGTFSNNNSRNCTIENPKREFPPIVYLIIFWGVLGNGLSIYVFLQPYKKSTSVNVF 60
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Qy          61 MLNLAISDLLFISTLPFRADYTLRGSNWIPGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
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Qy         121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
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Qy         301 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
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Db         301 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330


RESULT 2
ABU11900
ID   ABU11900 standard; Protein; 330 AA.
XX
AC   ABU11900;
XX
DT   13-FEB-2003  (first entry)
XX
DE   Human G-protein coupled receptor HGPRBMY11.
XX
KW   Human; receptor; HGPRBMY11; HGPRBMY11v1; HGPRBMY11v2; GPCR74; GPCR81;
KW   G-protein coupled receptor; cardiovascular disease; arrhythmia;
KW   myocardial infarction; congestive heart failure; cardiomyopathy;
KW   atherosclerosis; arteriosclerosis; embolism; angina; thrombosis;
KW   hypertension; Alzheimer's disease; Parkinson's disease; osteoporosis;
KW   obesity; human immunodeficiency virus infection; HIV; schizophrenia;
KW   sleeplessness; acquired immunodeficiency syndrome; AIDS; leukaemia;
KW   sepsis; inflammation; psoriasis; Gaucher's disease; ischaemia.
XX
OS   Homo sapiens.
XX
PN   WO200286123-A2.
XX
PD   31-OCT-2002.
XX
PF   16-NOV-2001; 2001WO-US44019.
XX
PR   17-NOV-2000; 2000US-249613P.
PR   21-DEC-2000; 2000US-257611P.
PR   16-JUL-2001; 2001US-305818P.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Peder J,  Nelson TC,  Ramanathan C,  Cacace AM,  Barber LE;
XX
DR   WPI; 2003-093137/08.
DR   N-PSDB; ABX56007.
XX
PT   New human G-protein coupled receptor HGPRBMY11 polypeptide or
PT   polynucleotide, useful for preventing, treating or ameliorating e.g.
PT   myocardial infarction, angina, thrombosis, Alzheimer's disease,
PT   schizophrenia, AIDS, leukemia -
XX
PS   Claim 11; Fig 1; 444pp; English.
XX
CC   The invention relates to an isolated polypeptide (designated HGPRBMY11),
CC   which has a G-protein coupled receptor (GPCR) activity (also known
CC   as GPCR74 or GPCR81) and is encoded by the cDNA contained in ATCC Deposit
CC   Number PTA-2766, its variants (HGPRBMY11v1 and HGPRBMY11v2), fragments,
CC   domains, species homologues and proteins 95% similar to it. Also included
CC   are: (1) the nucleic acids encoding the HGPRBMY11 proteins (including
CC   variants, fragments, complements and sequences 95% similar to the
CC   HGPRBMY11 nucleic acids); (2) recombinant vectors; (3) transformed host
CC   cells expressing HGPRBMY11; (4) an anti-HGPRBMY11 antibody; (5)
CC   diagnosing a pathological condition or a susceptibility to a pathological
CC   condition in a subject; (6) identifying a binding partner to the
CC   HGPRBMY11 polypeptide; (7) identifying an activity in a biological assay;
CC   (8) a process for making polynucleotide sequences encoding a gene product
CC   having altered GPCR activity; (9) a shuffled polynucleotide produced by
CC   the method of (8); and (10) screening for candidate compounds capable of
CC   binding to and/or modulating activity of a GPCR. The polypeptide or the
CC   polynucleotide is useful for preventing, treating or ameliorating a
CC   medical condition, particularly cardiovascular diseases or disorders,
CC   e.g. myocardial infarction, congestive heart failure, arrhythmias,
CC   cardiomyopathy, atherosclerosis, arteriosclerosis, embolism, angina,
CC   thrombosis or hypertension). The HGPRBMY11 polypeptide or polynucleotide
CC   is also useful for treating, preventing or ameliorating e.g. Alzheimer's
CC   disease, Parkinson's disease, osteoporosis, obesity, human
CC   immunodeficiency virus (HIV) infections, schizophrenia, sleeplessness,
CC   acquired immunodeficiency syndrome (AIDS), leukaemia, sepsis,
CC   inflammations, psoriasis, Gaucher's disease or ischaemia (many
CC   other diseases and disorders are listed in the specification)
CC   The present sequence represents an HGPRBMY11 protein (or variant).
XX
SQ   Sequence   330 AA;
```

```
  Query Match             100.0%;  Score 1712;  DB 24;  Length 330;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-177;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFPPIVYLIIFWGVLGNGLSIYVFLQPYKKSTSVNVF 60
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Db          1 MEPNGTFSNNNSRNCTIENFKREFPPIVYLIIFWGVLGNGLSIYVFLQPYKKSTSVNVF 60

Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120

Qy        121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180

Qy        181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240

Qy        241 FLCPLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACPNPLLYYPAGENFKDRL 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FLCPLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACPNPLLYYPAGENFKDRL 300

Qy        301 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
              |||||||||||||||||||||||||||||
Db        301 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330


RESULT 3
AAE07539
ID   AAE07539 standard; Protein; 341 AA.
XX
AC   AAE07539;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human G-protein coupled receptor 1b (GPCR1b) variant.
XX
KW   Human; G-protein coupled receptor; GPCRX; GPCR1b; cardiomyopathy;
KW   atherosclerosis; hypertension; congenital heart defect; anorexia;
KW   atrial septal defect; ventricular septal defect; valve disease;
KW   scleroderma; obesity; transplantation; adrenoleucodystrophy; AIDS;
KW   congenital adrenal hyperplasia; prostate cancer; lymphoma; cancer;
KW   haemophilia; idiopathic thrombocytopenic purpura; dyslipidaemia;
KW   acquired immune deficiency syndrome; diabetes; infectious disease;
KW   metabolic syndrome X; Albright Hereditary Osteodystrophy; ASD; VSD;
KW   neurodegenerative disorder; Alzheimer's disease; immune disorder;
KW   fertility; Parkinson's disorder; haematopoietic disorder;
KW   chromosome 13.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..54
FT                   /label= Signal_peptide
FT   Protein         55..341
FT                   /label= Mature_human_GPCR1b_protein_variant
XX
PN   WO200159113-A2.
XX
PD   16-AUG-2001.
XX
PF   08-FEB-2001; 2001WO-US04404.
XX
PR   08-FEB-2000; 2000US-0180929.
PR   08-FEB-2000; 2000US-0181045.
PR   09-FEB-2000; 2000US-0181157.
PR   09-FEB-2000; 2000US-0181339.
PR   09-FEB-2000; 2000US-0181344.
PR   09-FEB-2000; 2000US-0183392.
PR   17-FEB-2000; 2000US-0183611.
PR   20-JUL-2000; 2000US-0219585.
PR   20-JUL-2000; 2000US-0219758.
PR   26-JUL-2000; 2000US-0221341.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Taupier RJ, Burgess CE, Padigaru M, Tchernev VT, Mishra VS;
PI   Casman S, Ballinger R, Vernet CAM, Li L, Spytek KA, Andrew DP;
PI   Mezes PS;
XX
DR   WPI; 2001-497077/54.
DR   N-PSDB; AAD13709.
XX
PT   Novel G-protein coupled receptor proteins (GPCR1-GPCR-7) useful for
PT   treating or preventing, e.g., cardiomyopathy, atherosclerosis,
PT   hypertension, acquired immune deficiency syndrome, bronchial asthma,
PT   Crohn's disease, and multiple sclerosis -
XX
PS   Claim 1; Page 6; 135pp; English.
XX
CC   The invention relates to human G-protein coupled receptor proteins 1-7
CC   (GPCR1-7 or GPCRX) and nucleic acid molecules encoding such proteins.
CC   GPCRX sequences are used to treat or prevent a human suffering
CC   from GPCRX-associated disorders, e.g. cardiomyopathy, atherosclerosis,
CC   hypertension, congenital heart defects, aortic stenosis, atrial septal
CC   defect (ASD), atrioventricular (A-V) canal defect, ductus arteriosis,
CC   pulmonary stenosis, subaortic stenosis, ventricular septal defect
CC   (VSD), valve diseases, tuberous sclerosis, scleroderma, obesity,
CC   transplantation, adrenoleucodystrophy, congenital adrenal hyperplasia,
CC   prostate cancer, neoplasm, adenocarcinoma, lymphoma, uterus cancer,
CC   fertility, haemophilia, hypercoagulation, idiopathic thrombocytopenic
CC   purpura, graft versus host disease, acquired immune deficiency syndrome
CC   (AIDS), bronchial asthma, Crohn's disease, multiple sclerosis, and
CC   treatment of Albright Hereditary Osteodystrophy. GPCRX antibodies are
CC   used to treat a pathological state and treat or prevent disorders
CC   such as diabetes, metabolic disturbances associated with obesity,
CC   metabolic syndrome X, anorexia, wasting disorders associated with
CC   chronic diseases, infectious disease, cancer-associated cachexia,
CC   cancer, neurodegenerative disorders, Alzheimer's disease, Parkinson's
CC   disorder, immune disorders, haematopoietic disorders and various
CC   dyslipidaemias. GPCRX DNA is also useful in gene therapy. The present
CC   sequence is human GPCR1b protein variant. The GPCR1 DNA is located on
CC   chromosome 13.
XX
SQ   Sequence   341 AA;

  Query Match             100.0%;  Score 1712;  DB 22;  Length 341;
  Best Local Similarity   100.0%;  Pred. No. 5.7e-177;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFPPIVYLIIFWGVLGNGLSIYVFLQPYKKSTSVNVF 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 MEPNGTFSNNNSRNCTIENFKREFPPIVYLIIFWGVLGNGLSIYVFLQPYKKSTSVNVF 71

Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 131

Qy        121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 191

Qy        181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 251

Qy        241 FLCPLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACPNPLLYYPAGENFKDRL 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 FLCPLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACPNPLLYYPAGENFKDRL 311

Qy        301 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
              |||||||||||||||||||||||||||||
Db        312 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 341
```

```
RESULT 4
ABU11939
ID   ABU11939 standard; Protein; 341 AA.
XX
AC   ABU11939;
XX
DT   13-FEB-2003 (first entry)
XX
DE   Human G-protein coupled receptor HGPRBMY11v2.
XX
KW   Human; receptor; HGPRBMY11; HGPRBMY11v1; HGPRBMY11v2; GPCR74; GPCR81;
KW   G-protein coupled receptor; cardiovascular disease; arrhythmia;
KW   myocardial infarction; congestive heart failure; cardiomyopathy;
KW   atherosclerosis; arteriosclerosis; embolism; angina; thrombosis;
KW   hypertension; Alzheimer's disease; Parkinson's disease; osteoporosis;
KW   obesity; human immunodeficiency virus infection; HIV; schizophrenia;
KW   sleeplessness; acquired immunodeficiency syndrome; AIDS; leukaemia;
KW   sepsis; inflammation; psoriasis; Gaucher's disease; ischaemia.
XX
OS   Homo sapiens.
XX
PN   WO200286123-A2.
XX
PD   31-OCT-2002.
XX
PF   16-NOV-2001; 2001WO-US44019.
XX
PR   17-NOV-2000; 2000US-249613P.
PR   21-DEC-2000; 2000US-257619P.
PR   16-JUL-2001; 2001US-305818P.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Feder J, Nelson TC, Ramanathan C, Cascoe AM, Barber LE;
XX
DR   WPI; 2003-093137/08.
DR   N-PSDB; ABX56021.
XX
PT   New human G-protein coupled receptor HGPRBMY11 polypeptide or
PT   polynucleotide, useful for preventing, treating or ameliorating e.g.
PT   myocardial infarction, angina, thrombosis, Alzheimer's disease,
PT   schizophrenia, AIDS, leukemia -
XX
PS   Claim 33; Fig 15; 444pp; English.
XX
CC   The invention relates to an isolated polypeptide (designated HGPRBMY11),
CC   which has a G-protein coupled receptor (GPCR) (also known
CC   as GPCR74 or GPCR81) and is encoded by the cDNA contained in ATCC Deposit
CC   Number PTA-2766, its variants (HGPRBMY11v1 and HGPRBMY11v2), fragments,
CC   domains, species homologues and proteins 95% similar to it. Also included
CC   are: (1) the nucleic acids encoding the HGPRBMY11 proteins (including
CC   variants, fragments, complements and sequences 95% similar to the
CC   HGPRBMY11 nucleic acids); (2) recombinant vectors; (3) transformed host
CC   cells expressing HGPRBMY11; (4) an anti-HGPRBMY11 antibody; (5)
CC   diagnosing a pathological condition or a susceptibility to a pathological
CC   condition in a subject; (6) identifying a binding partner to the
CC   HGPRBMY11 polypeptide; (7) identifying an activity in a biological assay;
CC   (8) a process for making polynucleotide sequences encoding a gene product
CC   having altered GPCR activity; (9) a shuffled polynucleotide produced by
CC   the method of (8); and (10) screening for candidate compounds capable of
CC   binding to and/or modulating activity of a GPCR. The polypeptide or the
CC   polynucleotide is useful for preventing, treating or ameliorating a
CC   medical condition, particularly cardiovascular diseases or disorders,
CC   e.g. myocardial infarction, congestive heart failure, arrhythmias,
CC   cardiomyopathy, atherosclerosis, arteriosclerosis, embolism, angina,
CC   thrombosis or hypertension). The HGPRBMY11 polypeptide or polynucleotide
CC   is also useful for treating, preventing or ameliorating e.g. Alzheimer's
CC   disease, Parkinson's disease, osteoporosis, obesity, human
CC   immunodeficiency virus (HIV) infections, schizophrenia, sleeplessness,
CC   acquired immunodeficiency syndrome (AIDS), leukaemia, sepsis,
CC   inflammations, psoriasis, Gaucher's disease or ischaemia (many
CC   other diseases and disorders are listed in the specification).
CC   The present sequence represents an HGPRBMY11 protein (or variant).
XX
SQ   Sequence  341 AA;

  Query Match          100.0%;  Score 1712;  DB 24;  Length 341;
  Best Local Similarity  100.0%;  Pred. No. 5.7e-177;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEPNQTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 MEPNQTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 71

Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 131

Qy        121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 191

Qy        181 KLQTNMYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 KLQTNMYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 251

Qy        241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
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Db        252 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 311

Qy        301 KSALRKGHPQKATKCVFPVSVWLRKETRV 330
              |||||||||||||||||||||||||||||
Db        312 KSALRKGHPQKATKCVFPVSVWLRKETRV 341


RESULT 5
AAE12022
ID   AAE12022 standard; Protein; 346 AA.
XX
AC   AAE12022;
XX
DT   18-DEC-2001 (first entry)
XX
DE   Human G-protein coupled receptor, GCREC-1.
XX
KW   Human; G-protein coupled receptor; GCREC; gene therapy;
KW   proteosome analysis; cell proliferative disorder; arteriosclerosis;
KW   cancer; neurological disorder; Huntington's disease; Parkinson's disease;
KW   cardiovascular disorder; atherosclerosis; congestive heart failure;
KW   gastrointestinal disorder; gastritis; nausea; autoimmune; anaemia;
KW   inflammatory disorder; acquired immunodeficiency syndrome; AIDS;
KW   metabolic disorder; diabetes; obesity; viral infection; drug screening;
KW   chromosomal mapping; cytostatic; immunomodulatory; antiinflammatory;
KW   virucide.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..55
FT                   /label= Signal_peptide
FT   Domain          38..61
FT                   /label= Transmembrane_domain
FT   Domain          198..221
FT                   /label= Transmembrane_domain
FT   Protein         56..346
FT                   /note= 'Mature human GCREC-1 protein'
XX
PN   WO200172836-A2.
XX
PD   04-OCT-2001.
XX
PF   29-MAR-2001; 2001WO-US10436.
XX
PR   29-MAR-2000; 2000US-193051P.
PR   06-APR-2000; 2000US-195155P.
```

PR 20-APR-2000; 2000US-199084P.
PR 28-APR-2000; 2000US-200551P.
PR 05-MAY-2000; 2000US-202278P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Policky JL, Tribouley CM, Tang YT, Baughn MR, Graul R, Khan FA;
PI Nguyen DB, Patterson C, Lal P, Au-young J, Yang J, Hafalia A;
PI Walia NK, Das D;
XX
DR WPI; 2001-616472/71.
DR N-PSDB; AAD19577.
XX
PT New human G-protein coupled receptors, useful for treatment and
PT diagnosis of e.g. cell proliferation, also screening for specific
PT modulators, and related nucleic acid -
XX
PS Claim 1; Page 101-102; 111pp; English.
XX
CC The present sequence is a human G-protein coupled receptor, GCREC-1
CC protein. The GCRECs are used for treating or preventing disorders
CC associated with decreased expression of functional GCREC, and for
CC identifying specific agonists and antagonists, also binding agents
CC and modulators. They can also be used for generating specific antibodies
CC and for proteosome analysis. Disorders that can be treated include
CC cell proliferative disorders, e.g., arteriosclerosis and cancer,
CC neurological disorders, e.g., Huntington's disease and Parkinson's
CC disease, cardiovascular disorders, e.g., atherosclerosis and congestive
CC heart failure, gastrointestinal disorders, e.g., gastritis and nausea,
CC autoimmune/inflammatory disorders, e.g., acquired immunodeficiency
CC syndrome (AIDS) and anaemia, metabolic disorders, e.g., diabetes and
CC obesity and viral infections. Nucleic acids that encode GCREC are
CC used for identifying agents that alter its expression, for assessing
CC toxicity of test compounds, and as sources of primers and probes for
CC diagnostic detection of GCREC DNA and of therapeutic antisense and
CC ribozyme sequences. They can also be used in gene therapy, for
CC chromosomal mapping, and for recombinant production of GCREC. The
CC antibodies are useful for diagnosis and monitoring of diseases
CC associated with GCREC expression, for detecting and purifying GCREC,
CC and as therapeutic agents and for drug screening.
XX
SQ Sequence 346 AA;

Query Match 100.0%; Score 1712; DB 22; Length 346;
Best Local Similarity 100.0%; Pred. No. 5.8e-177;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIPFWGVLGNGLSIYVFLQPYKKSTSVNVF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIPFWGVLGNGLSIYVFLQPYKKSTSVNVF 76

Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMGYSLYVNMYSSIYFLTVLSVVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMGYSLYVNMYSSIYFLTVLSVVR 136

Qy        121 FLAMVHPFRLLHVTSIRSAWILCGIIWLLIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 FLAMVHPFRLLHVTSIRSAWILCGIIWLLIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 196

Qy        181 KLQTMNYIALVVGCLLPFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 KLQTMNYIALVVGCLLPFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 256

Qy        241 FLCFLPYHTLRTVHLTTKWGLCKDRLHKALVITLALAAANACFNPLLYYPAGENFKDRL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 FLCFLPYHTLRTVHLTTKWGLCKDRLHKALVITLALAAANACFNPLLYYPAGENFKDRL 316

Qy        301 KSALRKGHPQKAKTKCVPFVSVKLRKETRV 330
              |||||||||||||||||||||||||||||
Db        317 KSALRKGHPQKAKTKCVPFVSVKLRKETRV 346
```

RESULT 6

AAB82852
ID AAB82852 standard; Protein; 346 AA.
XX
AC AAB82852;
XX
DT 12-NOV-2001 (first entry)
XX
DE Human P2Y-like GPCR protein.
XX
KW P2Y-like; G-protein coupled receptor; GPCR; human;
KW cysteinyl leukotriene receptor; cysLT1 LTD4; bactericide;
KW fungicide; protozoacide; virucide; analgesic; cytostatic; anabolic;
KW antiasthmatic; antiparkinsonian; cardiant; hypertensive;
KW hypotensive; osteopathic; antiulcer; immunosuppressive;
KW antiallergic; antisclerotic; neuroprotective; antipsychotic;
KW therapy; vaccine.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 41..63
FT /label= TM1
FT /note= "transmembrane domain 1"
FT Domain 77..96
FT /label= TM2
FT /note= "transmembrane domain 2"
FT Domain 114..137
FT /label= TM3
FT /note= "transmembrane domain 3"
FT Domain 156..173
FT /label= TM4
FT /note= "transmembrane domain 4"
FT Domain 202..223
FT /label= TM5
FT /note= "transmembrane domain 5"
FT Domain 249..266
FT /label= TM6
FT /note= "transmembrane domain 6"
FT Domain 296..313
FT /label= TM7
FT /note= "transmembrane domain 7"
XX
PN WO200168842-A2.
XX
PD 20-SEP-2001.
XX
PF 13-MAR-2001; 2001WO-EP02785.
XX
PR 14-MAR-2000; 2000US-0189045.
XX
PA (FARB) BAYER AG.
XX
PI Xiao Y;
XX
DR WPI; 2001-565794/63.
DR N-PSDB; AAR26608.
XX
PT Nucleic acids encoding P2Y-like G-protein coupled receptor proteins,
PT useful for preventing diagnosing and treating, e.g. cancer, multiple
PT sclerosis, ulcers, bulimia and asthma -
XX
PS Claim 1(a); Fig 7; 110pp; English.
XX
CC The present sequence is that of a P2Y-like G-protein coupled receptor
CC (GPCR) that has 7 transmembrane regions. Homology searches showed
CC this receptor to be homologous to cysteinyl leukotriene
CC (cysLT1 LTD4) receptor and P2Y receptors. The invention provides
CC P2Y-like GPCR polypeptides and polynucleotides, expression vectors,
CC host cells, methods for detecting the polynucleotides, methods of
CC screening for agents which regulate or decrease the activity of a
CC P2Y-like GPCR protein, and a pharmaceutical composition comprising
CC an expression vector containing a P2Y-like GPCR polynucleotide
CC or a reagent that modulates a P2Y-like GPCR polypeptide or

```
CC  polynucleotide.  The pharmaceutical composition is used to modulate
CC  the activity of a P2Y-like GPCR in a disease, especially a
CC  bacterial, fungal, protozoan or viral infection, pain, cancer,
CC  anorexia, bulimia, chronic obstructive pulmonary disease, asthma,
CC  Parkinson's disease, acute heart failure, hypotension, hypertension,
CC  urinary retention, osteoporosis, angina pectoris, myocardial
CC  infarction, ulcer, allergy, multiple sclerosis, benign prostatic
CC  hypertrophy, a psychotic disorder, neurological disorder and
CC  dyskinesia (all claimed).
XX
SQ  Sequence  346 AA;

  Query Match             100.0%;  Score 1712;  DB 22;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-177;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFPWGVLGNGLSIYVFLQPYKKSTSVNVF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFPWGVLGNGLSIYVFLQPYKKSTSVNVF 76

Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 136

Qy        121 PLAMVHPFRLLHVTSIRSAWILCGIIWLLVAASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 PLAMVHPFRLLHVTSIRSAWILCGIIWLLVAASSIMLLDSGSEQNGSVTSCLELNLYKIA 196

Qy        181 KLQTWNYIALVVGCLLPFPLSICYLLIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 KLQTWNYIALVVGCLLPFPLSICYLLIRVLLKVEVPESGLRVSHRKALTTIITLIIF 256

Qy        241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYPAGENFKDRL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYPAGENFKDRL 316

Qy        301 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
              ||||||||||||||||||||||||||||||
Db        317 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 346


RESULT 7
AAE07538
ID  AAE07538 standard; protein; 346 AA.
XX
AC  AAE07538;
XX
DT  06-NOV-2001  (first entry)
XX
DE  Human G-protein coupled receptor 1a (GPCR1a) variant.
XX
KW  Human; G-protein coupled receptor; GPCRX; GPCR1a; cardiomyopathy;
KW  atherosclerosis; hypertension; congenital heart defect; anorexia;
KW  atrial septal defect; ventricular septal defect; valve disease;
KW  scleroderma; obesity; transplantation; adrenoleucodystrophy; AIDS;
KW  congenital adrenal hyperplasia; prostate cancer; lymphoma; cancer;
KW  haemophilia; idiopathic thrombocytopenic purpura; dyslipidaemia;
KW  acquired immune deficiency syndrome; diabetes; infectious disease;
KW  metabolic syndrome X; Albright Hereditary Osteodystrophy; ASD; VSD;
KW  neurodegenerative disorder; Alzheimer's disease; immune disorder;
KW  fertility; Parkinson's disorder; haematopoietic disorder.
XX
OS  Homo sapiens.
XX
FH  Key             Location/Qualifiers
FT  Peptide         1..59
FT                  /label= Signal_peptide
FT  Protein         60..346
FT                  /label= Mature_human_GPCR1a_protein_variant
XX
PN  WO200159113-A2.
XX
PD  16-AUG-2001.

XX
PF  08-FEB-2001; 2001WO-US04404.
XX
PR  08-FEB-2000; 2000US-0180929.
PR  08-FEB-2000; 2000US-0181045.
PR  09-FEB-2000; 2000US-0181157.
PR  09-FEB-2000; 2000US-0181339.
PR  09-FEB-2000; 2000US-0181344.
PR  09-FEB-2000; 2000US-0181392.
PR  17-FEB-2000; 2000US-0183191.
PR  20-JUL-2000; 2000US-0219585.
PR  20-JUL-2000; 2000US-0219758.
PR  26-JUL-2000; 2000US-0221341.
XX
PA  (CURA-) CURAGEN CORP.
XX
PI  Taupier RJ, Burgess CE, Padigaru M, Tchernev VT, Mishra VS;
PI  Casman S, Ballinger R, Vernet CAM, Li L, Spytek KA, Andrew DP;
PI  Mezes PS;
XX
DR  WPI; 2001-497077/54.
DR  N-PSDB; AAD13709.
XX
PT  Novel G-protein coupled receptor proteins (GPCR1-GPCR-7) useful for
PT  treating or preventing, e.g., cardiomyopathy, atherosclerosis,
PT  hypertension, acquired immune deficiency syndrome, bronchial asthma,
PT  Crohn's disease, and multiple sclerosis -
XX
PS  Claim 1; Page 6; 135pp; English.
XX
CC  The invention relates to human G-protein coupled receptor proteins 1-7
CC  (GPCR1-7 or GPCRX) and nucleic acid molecules encoding such proteins.
CC  GPCRX sequences are used to treat or prevent a human suffering
CC  from GPCRX-associated disorders, e.g. cardiomyopathy, atherosclerosis,
CC  hypertension, congenital heart defects, aortic stenosis, atrial septal
CC  defect (ASD), atrioventricular (A-V) canal defect, ductus arteriosis,
CC  pulmonary stenosis, subaortic stenosis, ventricular septal defect
CC  (VSD), valve diseases, tuberous sclerosis, scleroderma, obesity,
CC  transplantation, adrenoleucodystrophy, congenital adrenal hyperplasia,
CC  prostate cancer, neoplasm, adenocarcinoma, lymphoma, uterus cancer,
CC  fertility, haemophilia, hypercoagulation, idiopathic thrombocytopeuic
CC  purpura, graft versus host disease, acquired immune deficiency syndrome
CC  (AIDS), bronchial asthma, Crohn's disease, multiple sclerosis, and
CC  treatment of Albright Hereditary Osteodystrophy. GPCRX antibodies are
CC  used to treat a pathological state and treat or prevent disorders
CC  such as diabetes, metabolic disturbances associated with obesity,
CC  metabolic syndrome X, anorexia, wasting disorders associated with
CC  chronic diseases, infectious disease, cancer-associated cachexia,
CC  cancer, neurodegenerative disorders, Alzheimer's disease, Parkinson's
CC  disorder, immune disorders, haematopoietic disorders and various
CC  dyslipidaemias. GPCRX DNA is also useful in gene therapy. The present
CC  sequence is human GPCR1a protein variant.
XX
SQ  Sequence  346 AA;

  Query Match             100.0%;  Score 1712;  DB 22;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-177;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFPWGVLGNGLSIYVFLQPYKKSTSVNVF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFPWGVLGNGLSIYVFLQPYKKSTSVNVF 76

Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 136

Qy        121 PLAMVHPFRLLHVTSIRSAWILCGIIWLLVAASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 PLAMVHPFRLLHVTSIRSAWILCGIIWLLVAASSIMLLDSGSEQNGSVTSCLELNLYKIA 196

Qy        181 KLQTWNYIALVVGCLLPFPLSICYLLIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 KLQTWNYIALVVGCLLPFPLSICYLLIRVLLKVEVPESGLRVSHRKALTTIITLIIF 256

Qy        241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYPAGENFKDRL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYPAGENFKDRL 316

Qy        301 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
              ||||||||||||||||||||||||||||||
Db        317 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 346
```

```
Db        197 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 256

Qy        241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 316

Qy        301 KSALRKGHPQKAKTKCVPPVSVWLRKETRV 330
              |||||||||||||||||||||||||||||
Db        317 KSALRKGHPQKAKTKCVPPVSVWLRKETRV 346


RESULT 8
AAU04368
ID   AAU04368 standard; Protein; 346 AA.
XX
AC   AAU04368;
XX
DT   23-OCT-2001  (first entry)
XX
DE   Human G-protein coupled receptor, hRUP14.
XX
KW   Human; G-protein coupled receptor; GPCR; hRUP14; agonist;
KW   inverse agonist; lung cancer.
XX
OS   Homo sapiens.
XX
PN   WO200136471-A2.
XX
PD   25-MAY-2001.
XX
PF   16-NOV-2000; 2000WO-US31509.
XX
PR   17-NOV-1999;   99US-0166088.
PR   17-NOV-1999;   99US-0166099.
PR   17-NOV-1999;   99US-0166369.
PR   23-DEC-1999;   99US-0171900.
PR   23-DEC-1999;   99US-0171901.
PR   23-DEC-1999;   99US-0171902.
PR   11-FEB-2000;  2000US-0181749.
PR   14-MAR-2000;  2000US-0189258.
PR   14-MAR-2000;  2000US-0189259.
PR   10-APR-2000;  2000US-0195898.
PR   10-APR-2000;  2000US-0195899.
PR   10-APR-2000;  2000US-0196078.
PR   28-APR-2000;  2000US-0200419.
PR   12-MAY-2000;  2000US-0203630.
PR   12-JUN-2000;  2000US-0210741.
PR   12-JUN-2000;  2000US-0210982.
PR   21-AUG-2000;  2000US-0226760.
PR   26-SEP-2000;  2000US-0235418.
PR   26-SEP-2000;  2000US-0235779.
PR   20-OCT-2000;  2000US-0242332.
PR   20-OCT-2000;  2000US-0242343.
XX
PA   (AREN-) ARENA PHARM INC.
XX
PI   Chen R,  Dang HT,  Lowitz KP;
XX
DR   WPI; 2001-355616/37.
DR   N-PSDB; AAS07941.
XX
PT   Endogenous and non-endogenous versions of human G-protein coupled
PT   receptors for direct identification of candidate compounds as agonists,
PT   inverse agonists or partial agonists for use as therapeutic agents -
XX
PS   Claim 25; Page 100-101; 160pp; English.
XX
CC   The sequence represents a human G-protein coupled receptor (GPCR),
CC   hRUP14. The endogenous and non-endogenous, constitutively activated
CC   versions of human G-protein coupled receptors (GPCR), are useful for
CC   direct identification of candidate compounds as receptor agonists,
CC   inverse agonists or partial agonists having applicability as therapeutic
CC   agents for treating diseases related to GPCR, e.g. lung cancer.
CC   Non-endogenous version of human GPCRs are also utilized in research
CC   settings and in vitro and in vivo system, incorporating GPCRs can be
CC   utilised to elucidate and understand the roles these receptors
CC   play in the human condition, both normal and diseased.
XX
SQ   Sequence   346 AA;

  Query Match          100.0%;  Score 1712;  DB 22;  Length 346;
  Best Local Similarity  100.0%;  Pred. No. 5.8e-177;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEPNGTFSNNNSRNCTIENFKREPFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 MEPNGTFSNNNSRNCTIENFKREPFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 76

Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 136

Qy        121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSRQNGSVTSCLELNLYKIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSRQNGSVTSCLELNLYKIA 196

Qy        181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 256

Qy        241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 316

Qy        301 KSALRKGHPQKAKTKCVPPVSVWLRKETRV 330
              |||||||||||||||||||||||||||||
Db        317 KSALRKGHPQKAKTKCVPPVSVWLRKETRV 346


RESULT 9
AAU07294
ID   AAU07294 standard; Protein; 346 AA.
XX
AC   AAU07294;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Cysteinyl leukotriene receptor HIPHUM0000007.
XX
KW   Cysteinyl leukotriene receptor; HIPHUM0000007; antiasthmatic; antiHIV;
KW   antiallergic; antiinflammatory; antiarteriosclerotic; antiarrhythmic;
KW   vasotropic; cytostatic; neuroprotective; antirheumatoid; antiarthritic;
KW   immunosuppressive; antipsoriatic; dermatological; antibacterial;
KW   cerebroprotective; antithyroid; asthma; allergic rhinitis; AIDS;
KW   cardiac arrhythmia; myocardial ischaemia; atherosclerosis; heart failure;
KW   rheumatoid arthritis; immune disorder; dermatitis; septic shock; stroke.
XX
OS   Homo sapiens.
XX
PN   WO200159105-A1.
XX
PD   16-AUG-2001.
XX
PF   12-FEB-2001; 2001WO-GB00560.
XX
PR   10-FEB-2000; 2000GB-0003079.
XX
PA   (GLAX ) GLAXO GROUP LTD.
XX
PI   Cousens DJ,  Volpe F,  Igner DM;
XX
DR   WPI; 2001-514666/56.
DR   N-PSDB; AAS10778.
XX
PT   Novel cysteinyl leukotriene receptor polypeptide, termed as
PT   HIPHUM0000007 polypeptide, useful for treating cardiovascular diseases,
```

```
PT   lung diseases, allergic rhinitis, immune deficiency and disorder -
XX
PS   Claim 1; Page 47-48; 52pp; English.
XX
CC   The sequence represents the amino acid sequence of cysteinyl leukotriene
CC   receptor polypeptide, termed as HIPHUM0000007. The nucleic acid is useful
CC   for identifying a substance that modulates cysteinyl leukotriene receptor
CC   activity. This substance is useful for treating a subject having a
CC   disorder which is responsive to cysteinyl leukotriene receptor
CC   modulation, such as asthma, chronic obstructive pulmonary disease (COPD),
CC   allergic rhinitis, cardiac arrhythmia, myocardial ischemia,
CC   atherosclerosis and heart failure. It is also useful in the therapeutic
CC   treatment and/or prophylaxis of disorders such as acquired immune
CC   deficiency syndrome (AIDS), rheumatoid arthritis, multiple sclerosis,
CC   leukaemia, myasthenia gravis, Grave's disease, systemic lupus
CC   erythematosus, inflammatory bowel disease, encephalomyelitis, psoriasis,
CC   atopic dermatitis, septic shock, stroke and ischaemia reperfusion injury.
CC   The antibody to cysteinyl leukotriene receptor is useful for
CC   immunoprecipitation techniques, as tools to further elucidate the
CC   function of HIPHUM0000007 or its variant, and as therapeutic agent. The
CC   nucleic acid is useful for identifying mutations in HIPHUM0000007 gene
CC   implicated in human disorders, which is in turn useful for diagnosing the
CC   disorder or susceptibility to the disorder and in assessing the
CC   physiology of the disorders. It is also useful in hybridisation studies
CC   to monitor up- or down-regulation of HIPHUM0000007 expression.
XX
SQ   Sequence  346 AA;

  Query Match             100.0%;  Score 1712;  DB 22;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-177;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFPPIVYLLIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 MEPNGTFSNNNSRNCTIENFKREFPPIVYLLIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 76

Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 136

Qy        121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 196

Qy        181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 256

Qy        241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 316

Qy        301 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
              |||||||||||||||||||||||||||||
Db        317 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 346


RESULT 10
AAB73097
ID   AAB73097 standard; Protein; 346 AA.
XX
AC   AAB73097;
XX
DT   05-JUN-2001  (first entry)
XX
DE   Human LTC4 receptor SEQ ID NO: 2.
XX
KW   Human; peptide leukotriene receptor; LTC4; allergy;
KW   inflammatory disorder.
XX
OS   Homo sapiens.
XX
PN   WO200119986-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-JP06265.
XX
PR   14-SEP-1999;  99JP-0259986.
XX
PA   (YAMA ) YAMANOUCHI PHARM CO LTD.
PA   (HELI-) HELIX RES INST.
XX
PI   Takasaki J,  Kamohara M,  Matsumoto M,  Saito T,  Sugimoto T,  Ota T;
PI   Isogai T,  Nishikawa T,  Kawai Y;
XX
DR   WPI; 2001-244800/25.
DR   N-PSDB; AAF81528.
XX
PT   New leukotriene C4 receptor protein for screening modifiers of ligand
PT   binding activity for treating allergic and inflammatory disorders, such
PT   as ulcerative colitis and asthma -
XX
PS   Claim 1; Page 63-64; 83pp; Japanese.
XX
CC   The present invention provides the protein and coding sequences of a
CC   novel human, pig and rat leukotriene C4 receptor. These sequences can
CC   be used to screen for substances that can be used in the treatment and
CC   prevention of allergic and inflammatory disorders including dermatitis,
CC   inflammatory bowel disease, ulcerative colitis, asthma and bronchitis.
CC   The present sequence is the human LTC4 receptor.
XX
SQ   Sequence  346 AA;

  Query Match             100.0%;  Score 1712;  DB 22;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-177;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFPPIVYLLIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 MEPNGTFSNNNSRNCTIENFKREFPPIVYLLIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 76

Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 136

Qy        121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 196

Qy        181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 256

Qy        241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 316

Qy        301 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
              |||||||||||||||||||||||||||||
Db        317 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 346


RESULT 11
ABP95624
ID   ABP95624 standard; Protein; 346 AA.
XX
AC   ABP95624;
XX
DT   06-MAR-2003  (first entry)
XX
DE   Human GPCR polypeptide SEQ ID NO 58.
XX
KW   Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
KW   drug development; gustatory; taste; fragrance; receptor.
XX
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```
OS   Homo sapiens.
XX
PN   WO200216548-A2.
XX
PD   28-FEB-2002.
XX
PF   30-JUL-2001; 2001WO-IB01446.
XX
PR   04-AUG-2000; 2000JP-0237818.
PR   13-FEB-2001; 2001JP-0034434.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Haga T, Takeda S, Mitaku S;
XX
DR   WPI; 2002-304118/34.
DR   N-PSDB; ABZ42898.
XX
PT   Database global search for G protein-coupled receptors, proteins and
PT   encoded genes for studying in vivo signal transduction mechanism and
PT   identifying targets for drug development -
XX
PS   Claim 10; SEQ ID NO 58; 97pp + Sequence Listing; Japanese.
XX
CC   The invention relates to a method for screening G protein-coupled
CC   receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins
CC   (ABP95596-ABP95942) by extracting open-reading frames containing 6-8
CC   transmembrane domains with 250-1000 amino acid residues to give a gene
CC   homologous with a known GPCR gene. The receptor proteins and encoded
CC   genes are useful for studying in vivo signal transduction mechanism and
CC   identifying targets for drug development e.g. based on olfactory and
CC   gustatory receptors in form of agonists and antagonists by screening
CC   intrinsic and extrinsic ligands as bitter taste inhibitors, taste
CC   enhancers and fragrance improvers.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence  346 AA;

  Query Match             100.0%;  Score 1712;  DB 23;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-177;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFPPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 MEPNGTFSNNNSRNCTIENFKREFPPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 76

Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSTSLYVNMYSSIYFLTVLSVVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSTSLYVNMYSSIYFLTVLSVVR 136

Qy        121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 196

Qy        181 KLQTMNYIALVVGCLLPFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 KLQTMNYIALVVGCLLPFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 256

Qy        241 FLCFLPYTHTLRTVHLTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 FLCFLPYTHTLRTVHLTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 316

Qy        301 KSALRKGHPQKAKTKCVPPVSVWLRKETRV 330
              ||||||||||||||||||||||||||||||
Db        317 KSALRKGHPQKAKTKCVPPVSVWLRKETRV 346


RESULT 12
ABG66684
ID   ABG66684 standard; Protein; 346 AA.
XX
AC   ABG66684;
XX
DT   30-AUG-2002  (first entry)
XX
DE   Human novel polypeptide #19.
XX
KW   Human; inflammatory condition; shock; sepsis; immune response;
KW   cancer; wound healing; central nervous system disease; haematopoiesis;
KW   peripheral nervous system disease; amyotrophic lateral sclerosis; tendon;
KW   myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone;
KW   cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis;
KW   bone degenerative disorder; periodontal disease; reperfusion injury;
KW   lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection;
KW   allergic condition; thrombolysis; thrombosis; coagulation disorder;
KW   fungal infection.
XX
OS   Homo sapiens.
XX
PN   WO200204340-A2.
XX
PD   06-JUN-2002.
XX
PF   30-NOV-2001; 2001WO-US47004.
XX
PR   30-NOV-2000; 2000US-0028952.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Wang J, Wang D;
PI   Yamazaki V, Ujwal ML, Drmanac RT;
XX
DR   WPI; 2002-508509/54.
DR   N-PSDB; ABK94908.
XX
PT   Novel nucleic acids and polypeptides for diagnosis, treatment of
PT   inflammatory, autoimmune, nervous system, myeloid or lymphoid cell
PT   disorders, cancer and promoting wound healing -
XX
PS   Claim 10; Page 582-583; 672pp; English.
XX
CC   The invention relates to human novel polynucleotides and associated
CC   polypeptides. The polynucleotides and polypeptides are useful for
CC   treating inflammatory conditions such as arthritis, nephritis, Crohn's
CC   disease, ischaemia-reperfusion injury, shock, sepsis, immune responses
CC   against cancer and for promoting wound healing. The sequences are used to
CC   induce the proliferation of neural cells and regeneration of nerve and
CC   brain tissue, and are useful for the treatment of central and peripheral
CC   nervous system diseases and neuropathies, such as Alzheimer's disease,
CC   Parkinson's disease, Huntington's disease and amyotrophic lateral
CC   sclerosis. The sequences are involved in chemotactic or chemokinetic
CC   activity, regulation of haematopoiesis, treatment of myeloid or lymphoid
CC   cell disorders and platelet disorders such as thrombocytopenia,
CC   regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
CC   growth, tissue repair, healing of burns, incisions, ulcers, treatment of
CC   osteoporosis, osteoarthritis, bone degenerative disorders and periodontal
CC   disease. The sequences of the invention are also useful for gut
CC   protection or regeneration and treatment of lung or liver fibrosis,
CC   reperfusion injury in various tissues, immune deficiencies and disorders
CC   including severe combined immunodeficiency (SCID), bacterial or fungal
CC   infections, autoimmune disorders e.g. multiple sclerosis and myasthenia
CC   gravis, allergic conditions such as asthma, thrombolysis or thrombosis
CC   and coagulation disorders. Sequences ABG66666-ABG66758 represent human
CC   novel polypeptides of the invention.
XX
SQ   Sequence  346 AA;

  Query Match             100.0%;  Score 1712;  DB 23;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-177;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFPPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 MEPNGTFSNNNSRNCTIENFKREFPPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 76
```

```
Qy          61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          77 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 136

Qy         121 FLAMVHPFRLLHVTSISRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         137 FLAMVHPFRLLHVTSISRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 196

Qy         181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         197 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 256

Qy         241 FLCPLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACPNPLLYYFAGENFKDRL 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         257 FLCPLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACPNPLLYYFAGENFKDRL 316

Qy         301 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
               |||||||||||||||||||||||||||||
Db         317 KSALRKGHPQKAKTKCVFPVSWLRKETRV 346
```

RESULT 13
AAU10004
ID AAU10004 standard; protein; 346 AA.
XX
AC AAU10004;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human CysLT2-like G-protein coupled receptor protein.
XX
KW CysLT2; G-protein coupled receptor; GPCR; cysteinylleukotriene2;
KW antibacterial; fungicide; virucide; cytostatic; anti-HIV; antianginal;
KW hypotensive; hypertensive; osteopathic; tranquiliser; nootropic;
KW anti-inflammatory; neuroprotective; antiparkinsonian; analgesic;
KW cardiant; cerebroprotective; antiasthmatic; antiallergic; antiarthritic;
KW antiulcer; antibody; immunogen; bacterial infection; fungal infection;
KW viral infection; human immunodeficiency virus; HIV; cancer; anorexia;
KW bulimia; cardiovascular disease; acute heart failure; angina;
KW myocardial infarction; ulcer; osteoporosis; asthma; allergy; neurogenic;
KW myopathic; neurodegenerative; Alzheimer's disease; Parkinson's disease;
KW motor neuron disease; dementia; inflammatory disease; arthritis;
KW multiple sclerosis; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 41..63
FT /note= "Transmembrane helix"
FT Domain 77..96
FT /note= "Transmembrane helix"
FT Domain 93..110
FT /note= "Transmembrane helix"
FT Region 104..143
FT /note= "GPCR region"
FT Domain 113..137
FT /note= "Transmembrane helix"
FT Domain 115..139
FT /note= "Transmembrane helix"
FT Domain 156..173
FT /note= "Transmembrane helix"
FT Domain 202..223
FT /note= "Transmembrane helix"
FT Region 210..221
FT /note= "GPCR region"
FT Region 241..268
FT /note= "GPCR region"
FT Domain 250..266
FT /note= "Transmembrane helix"
FT Domain 291..313
FT /note= "Transmembrane helix"
FT Region 297..308
FT /note= "GPCR region"
XX
PN WO200177149-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-EP03981.
XX
PR 07-APR-2000; 2000US-195196P.
PR 13-DEC-2000; 2000US-254876P.
XX
PA (FARB) BAYER AG.
XX
PI Xiao Y;
XX
DR WPI; 2002-049130/06.
DR N-PSDB; AAS16243.
XX
PT New polypeptide, useful for treating peripheral or central nervous
PT system, cardiovascular diseases and asthma, comprises the human
PT cysteinylleukotriene2-like G protein-coupled receptor polypeptide
XX
PS Claim 25; Fig 9; 136pp; English.
XX
CC This sequence represents a human CysL2-like G-protein coupled receptor
CC (GPCR) protein of the invention. The invention comprises the DNA and
CC protein sequences of an isolated human CysLT2 (cysteinylleukotriene2)-
CC like G protein-coupled receptor (GPCR) protein. This protein may have
CC antibacterial, fungicide, virucide, cytostatic, anti -HIV, antianginal,
CC hypotensive, hypertensive, osteopathic, tranquiliser, nootropic, anti-
CC inflammatory, neuroprotective, antiparkinsonian, analgesic, cardiant,
CC cerebroprotective, antiasthmatic, antiallergic, antiarthritic and
CC antiulcer activities. The invention also comprises an agent which
CC inhibits the function of the CysLT2-like protein and is useful for
CC treating CysLT2-like GPCR disorders. The protein or its fragment are
CC useful in raising specific antibodies which can block ligand binding,
CC and are useful for treating disorders such as bacterial, fungal and
CC viral infections and particularly those caused by human immunodeficiency
CC (HIV) virus, cancers, anorexia, bulimia, cardiovascular diseases (e.g.
CC acute heart failure, angina, myocardial infarction), ulcers,
CC osteoporosis, asthma, allergies, central and peripheral nervous system
CC disease, a disease of the motor unit like neurogenic and myopathic
CC disorders, neurodegenerative disorders (e.g. Alzheimer's and Parkinson's
CC disease, motor neuron disease, dementia) also inflammatory diseases of
CC the nervous system (e.g. arthritis and multiple sclerosis). The
CC coding sequence of CysLT2-like GPCR polynucleotide is useful for
CC generating antisense oligonucleotides or ribozymes which specifically
CC bind to mRNA transcribed from the cysLT2 gene and are useful for
CC modulating CysLT2-like GPCR gene expression.
XX
SQ Sequence 346 AA;

```
  Query Match          100.0%;  Score 1712;  DB 23;  Length 346;
  Best Local Similarity  100.0%;  Pred. No. 5.8e-177;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFPPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 MEPNGTFSNNNSRNCTIENFKREFPPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 76

Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 136

Qy        121 FLAMVHPFRLLHVTSISRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 FLAMVHPFRLLHVTSISRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 196

Qy        181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 256

Qy        241 FLCPLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACPNPLLYYFAGENFKDRL 300
```

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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          257 FLCFLPYHTLRTVHLTTNKVGLCKDRLHKALVITLALAAAANACFNPLLYYFAGENFKDRL 316

Qy          301 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
                ||||||||||||||||||||||||||||||
Db          317 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 346


RESULT 14
AAE17231
ID   AAE17231 standard; Protein; 346 AA.
XX
AC   AAE17231;
XX
DT   07-MAY-2002  (first entry)
XX
DE   Human CysLT2 GPCR (G-protein coupled receptor).
XX
KW   Human; CysLT2 GPCR; G-protein coupled receptor; oedema; asthma;
KW   immunological disorder; vascular disorder; reproductive disease;
KW   cellular metabolism; growth, development; blood; bone homeostasis;
KW   inflammation; allergy; angiogenesis; respiratory distress syndrome;
KW   Crohn's disease; blood pressure; protein therapy; anti-inflammatory;
KW   inflammatory disorder.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          1..41
FT                   /label= Extracellular_domain
FT   Modified-site   20..22
FT                   /note= "N-glycosylation site"
FT   Modified-site   26..28
FT                   /note= "N-glycosylation site"
FT   Domain          94..115
FT                   /note= "Extracellular domain between the second and
FT                   third transmembrane domains"
FT   Domain          175..203
FT                   /note= "Extracellular domain between the fourth and
FT                   fifth transmembrane domains"
FT   Modified-site   181..183
FT                   /note= "N-glycosylation site"
FT   Domain          268..289
FT                   /note= "Extracellular domain between the sixth and
FT                   seventh transmembrane domains"
XX
PN   WO200192302-A2.
XX
PD   06-DEC-2001.
XX
PF   25-MAY-2001; 2001WO-US16965.
XX
PR   26-MAY-2000; 2000US-207725P.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Murphy A.  Martin J;
XX
DR   WPI; 2002-154523/20.
DR   N-PSDB; AAD28591.
XX
PT   New HUMAN CysLT2 GPCR (G-protein coupled receptor), useful for
PT   diagnosing, preventing and treating inflammatory, immunological or
PT   vascular disorders, e.g. asthma, allergy, angiogenesis, Crohn's disease
PT   or edema  -
XX
PS   Claim 2; Fig 1A-1C; 58pp; English.
XX
CC   The invention relates to human CysLT2 GPCR (G-protein coupled receptor)
CC   polypeptide and its corresponding nucleic acid. The human CysLT2 GPCR,
CC   antibodies and compositions are useful for treating the human or animal
CC   body, or for diagnosing a disease. Human CysLT2 GPCR is useful for
CC   diagnosing, preventing and treating inflammatory, immunological,
CC   vascular disorders, reproductive diseases, or diseases related to
CC   cellular metabolism, growth, development, blood and bone homeostasis.
CC   These disorders or diseases include asthma, inflammation, allergy,
CC   angiogenesis, respiratory distress syndrome, Crohn's disease, oedema,
CC   high or low blood pressure growth, development, blood and bone
CC   homeostasis. Human CysLT2 GPCR is also used in protein therapy. The
CC   present sequence is human CysLT2 GPCR protein.
XX
SQ   Sequence  346 AA;

  Query Match             100.0%;  Score 1712;  DB 23;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-177;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFPPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVWVF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 MEPNGTFSNNNSRNCTIENFKREFPPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVWVF 76

Qy         61 MLNLAISDLLFISTLFPRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 MLNLAISDLLFISTLFPRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 136

Qy        121 FLAMVHPFRLLFVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 FLAMVHPFRLLFVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 196

Qy        181 KLQTMNYIALVVGCLLPFTTLSICYLLIRVLLKVEVPESGLRVSHRKALTTIITLLIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 KLQTMNYIALVVGCLLPFTTLSICYLLIRVLLKVEVPESGLRVSHRKALTTIITLLIF 256

Qy        241 FLCFLPYHTLRTVHLTTNKVGLCKDRLHKALVITLALAAAANACFNPLLYYFAGENFKDRL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 FLCFLPYHTLRTVHLTTNKVGLCKDRLHKALVITLALAAAANACFNPLLYYFAGENFKDRL 316

Qy        301 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
              ||||||||||||||||||||||||||||||
Db        317 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 346


RESULT 15
AAG77965
ID   AAG77965 standard; Protein; 346 AA.
XX
AC   AAG77965;
XX
DT   25-FEB-2002  (first entry)
XX
DE   Human G-protein coupled receptor PPI-017*.
XX
KW   Human; G-protein coupled receptor; GPCR; PPI-017*; cytostatic;
KW   antiallergic; osteopathic; cardiovascular; immunosuppressive; neoplastic;
KW   gene therapy; heart disease; gastrointestinal disease; sleep disorder;
KW   immunological disorder; pulmonary disorder; infectious disease;
KW   myeloproliferative disease; allergic rhinitis; asthma; COPD; obesity;
KW   chronic obstructive pulmonary disease; inflammatory bowel disease;
KW   diabetes; metabolic disease; neurological disease; urogenital disease;
KW   inflammation; cancer; osteoporosis; cardiovascular disease; infection;
KW   allergy; respiratory disease; sensory organ disorder; hair loss;
KW   immunological disorder; pulmonary disease; neoplastic disease;
KW   vasculitic granulomatous disease; dermatology; psychotherapeutic.
XX
OS   Homo sapiens.
XX
PN   US2001039037-A1.
XX
PD   08-NOV-2001.
XX
PF   05-APR-2001; 2001US-0826791.
XX
PR   05-APR-2000; 2000GB-0008504.
PR   19-APR-2000; 2000US-198367P.
XX
PA   (HARL/) HARLAND L.
```

XX
PI Harland L;
XX
DR WPI; 2002-040722/05.
DR N-PSDB; AAH77279.
XX
PT New PFI-017 protein and polynucleotide encoding the protein, useful for
PT diagnosing or treating metabolic diseases, urogenital disease,
PT immunological disorders, infectious diseases, neoplastic or
PT myeloproliferative diseases
XX
PS Claim 7; Fig 7B; 39pp; English.
XX
CC The sequence represents a novel G-protein coupled receptor (GPCR),
CC PFI-017* of the invention. The PFI-017 has cytostatic, antiallergic,
CC osteopathic, cardiovascular, and immunosuppressive activity. The
CC polynucleotides may have a use in gene therapy. The polynucleotide is
CC useful for treating allergic disorders, an inflammatory disorder, an
CC immunological disorder, a pulmonary disorder, an infectious disease, a
CC neoplastic or myeloproliferative disease, or a heart disease. The
CC allergic disorder is an allergic rhinitis or asthma, the pulmonary
CC disease is COPD, and the inflammatory disorder is inflammatory bowel
CC disease. PFI-017 polynucleotide sequences may be used for the diagnosis
CC of diseases resulting from expression of PFI-017, and to detect and
CC quantify gene expression in conditions, disorders or diseases in which
CC PFI-017 activity may be implicated. The polypeptides are used to produce
CC anti-PFI-017 antibodies to be used diagnostically to detect and quantify
CC PFI-017 levels in disease states. The antibodies, compounds and
CC compositions which can modulate the peptide can be used in treating
CC obesity, diabetes and metabolic disease, neurological disease, urogenital
CC disease, inflammation, cancer, osteoporosis, cardiovascular disease,
CC gastrointestinal disease, infections, allergy and respiratory disease,
CC sensory organ disorders, sleep disorders, hair loss, immunological
CC disorders, pulmonary diseases, infectious diseases, neoplastic and
CC myeloproliferative diseases, vasculitic granulomatous diseases, and heart
CC diseases. These may also be used in dermatology, and psychotherapeutics.
XX
SQ Sequence 346 AA;

Query Match 100.0%; Score 1712; DB 23; Length 346;
Best Local Similarity 100.0%; Pred. No. 5.8e-177;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MEPWGTFSNNNSRNCTIENPKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVF 76

Qy         61 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 MLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 136

Qy        121 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 196

Qy        181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 256

Qy        241 FLCFLPYHTLRTVHLFTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFACENFKDRL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 316

Qy        301 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330
              ||||||||||||||||||||||||||||||
Db        317 KSALRKGHPQKAKTKCVFPVSVWLRKETRV 346
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Search completed: October 8, 2003, 08:32:03
Job time : 87 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 8, 2003, 08:26:59 ; Search time 40 Seconds
(without alignments)
793.392 Million cell updates/sec

Title: US-09-991-225-2
Perfect score: 1712
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	467	27.3	362	2	S33733	G protein-coupled
2	447	26.1	308	2	I50241	G protein-coupled
3	446	26.1	373	2	JC4737	G protein-coupled
4	442	25.8	373	2	JC4162	P2Y receptor - bov
5	440	25.7	361	2	B45680	G protein-coupled
6	436	25.5	344	2	T09508	intron 17 purinerg
7	430	25.1	370	2	JC5549	heptahelical P2Y5-
8	418.5	24.4	373	2	A47556	ATP receptor P2u -
9	416	24.3	342	2	S13638	platelet-activatin
10	416	24.3	375	2	A54946	P-2U nucleotide re
11	409.5	23.9	342	2	A40191	platelet-activatin
12	404.5	23.6	420	2	I51667	thrombin receptor
13	404	23.6	341	2	S63666	platelet activatin
14	400.5	23.4	397	2	S66518	proteinase-activat
15	398	23.2	380	2	I38435	angiotensin recept
16	397	23.2	341	2	S43252	platelet-activatin
17	394.5	23.0	355	2	A45177	chemokine (C-C) re
18	391	22.8	328	2	I55450	G protein-coupled
19	390.5	22.8	355	2	I49339	macrophage inflamm
20	390	22.8	399	2	I48705	proteinase activat
21	387	22.6	371	2	JC5796	probable chemoattr
22	382	22.3	371	2	JC5498	G protein-coupled
23	378.5	22.1	378	2	B55735	lymphocyte-specifi
24	378	22.1	355	2	JC5067	G protein-coupled
25	376	22.0	356	2	I49340	MIP-1 alpha recept
26	373.5	21.8	387	2	I69202	G protein-coupled
27	372.5	21.8	363	2	I57955	somatostatin recep
28	372.5	21.8	364	2	JN0763	somatostatin recep
29	372.5	21.8	378	2	A55735	G protein-coupled
30	372	21.7	363	2	I57940	somatostatin recep
31	371.5	21.7	365	2	S68208	G protein-coupled
32	370.5	21.6	383	2	S55594	G protein-coupled
33	370	21.6	365	2	S68679	G protein-coupled
34	366	21.4	355	2	G02436	chemokine (C-C) re
35	366	21.4	427	2	S17148	alpha-thrombin rec
36	364.5	21.3	362	2	JN0694	angiotensin II rec
37	363	21.2	359	2	S15403	angiotensin II rec
38	361.5	21.1	352	2	A43113	chemokine (C-C) re
39	360	21.0	432	2	A43448	thrombin receptor
40	357	20.9	328	2	JC4800	P2Y6 receptor - hu
41	356.5	20.8	333	2	I65989	G protein-coupled
42	356.5	20.8	361	2	JC5653	G protein-coupled
43	356.5	20.8	378	2	A45680	G protein-coupled
44	356	20.8	359	2	A48857	angiotensin II rec
45	356	20.8	363	2	A49092	angiotensin II rec

ALIGNMENTS

RESULT 1
S33733
G protein-coupled receptor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999
C;Accession: S33733
R;Webb, T.E.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burr
FEBS Lett. 324, 219-225, 1993
A;Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor
A;Reference number: S33733; MUID:93285340; PMID:8508924
A;Accession: S33733
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-362 <WEB>
A;Cross-references: EMBL:X73268; NID:g395084; PIDN:CAA51716.1; PID:g395085
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein

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  Query Match             27.3%;  Score 467;  DB 2;  Length 362;
  Best Local Similarity   30.7%;  Pred. No. 1.3e-31;
  Matches   98;  Conservative   83;  Mismatches  112;  Indels   26;  Gaps    7;

Qy          5 GTFSNNNSRNCTI--ENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFML 62
              |  : | :  |::    |:  : | |:::|  | ||| ::|::|:   :  : ::|:|
Db         21 GWAAGNATTKCSLTKTGFQFYYLPTVYILVFITGFLGNSVAIWMFVFHMRPWSGISVYMF 80

Qy         63 NLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFL 122
              |||::| |:: |||      ||    ::|||||: |::   :   :||:| || ||| :|| |:
Db         81 NLALADFLYVLTLPALIFYYFNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISVHRYT 140

Qy        123 AMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLL---DSGSEQNGSVTSCLE------ 173
               :||| : |      ::|  :  ::| |::|     :|    :|  :| ::| | :
Db        141 GVVHPLKSLGRLKKKNAVYVSSLVWALVVAVIAPILFYSGTGVRRNKTIT-CYDTTADEY 199

Qy        174 LNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTI 233
              |  | :  : |  ::  :     ||  :  || ||:: |:  ::  | ||   ||::  :
Db        200 LRSYFVYSMCTTVFMFCI-----PFIVILGCYGLIVKALIYKDLDNSPLR---RKSIYLV 251

Qy        234 IITLIIFFLCFLPYHTLRTVHL------TTWKVGLCKDRLHKALVITLALAAANACFNPL 287
              || | :| : :||:| ::|::|       | ::     |:::     :|  ||: |:| :|:
Db        252 IIVLTVFAVSYLPFHVMKTLNLRARLDFQTPQMCAFNDKVYATYQVTRGLASLNSCVDPI 311

Qy        288 LYYFAGENFKDRLKSALRK 306
              ||: ||: |: ||  | ||
Db        312 LYFLAGDTFRRRLSRATRK 330
```

RESULT 2
I50241
G protein-coupled receptor 6H1 - chicken
N;Alternate names: purinoceptor 6H1
C;Species: Gallus gallus (chicken)

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 02-Jun-2000
C;Accession: I50241; JC4618
R;Kaplan, M.H.; Smith, D.I.; Sundick, R.S.
J. Immunol. 151, 628-636, 1993
A;Title: Identification of a G protein coupled receptor induced in activated T cells.
A;Reference number: I50241; MUID:93329058; PMID:8393036
A;Accession: I50241
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-308 <KAP>
A;Cross-references: GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:g304384
R;Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
Biochem. Biophys. Res. Commun. 219, 105-110, 1996
A;Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.
A;Reference number: JC4618; MUID:96190677; PMID:8619790
A;Accession: JC4618
A;Molecule type: mRNA
A;Residues: 1-308 <WEB>
A;Cross-references: GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:g304384
A;Experimental source: T-cells
C;Comment: This receptor plays a role in T-cell activation.
C;Genetics:
A;Gene: p2Y5
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
F;15-40/Domain: transmembrane #status predicted <TM1>
F;51-74/Domain: transmembrane #status predicted <TM2>
F;89-109/Domain: transmembrane #status predicted <TM3>
F;133-153/Domain: transmembrane #status predicted <TM4>
F;177-201/Domain: transmembrane #status predicted <TM5>
F;227-248/Domain: transmembrane #status predicted <TM6>
F;269-292/Domain: transmembrane #status predicted <TM7>

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  Query Match             26.1%;  Score 447;  DB 2;  Length 308;
  Best Local Similarity   35.4%;  Pred. No. 5.1e-30;
  Matches  105;  Conservative   53;  Mismatches  119;  Indels   20;  Gaps    8;

Qy         12 SRNCTIE-NFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLL 70
              | ||: | :||    :  |: ::|  |:: | ::||:|     |         :||||||||||
Db          3 SSNCSTEDSFKYTLYGCVFSMVFVLGLIANCVAIYIFTFTLKVRNETTTYMLNLAISDLL 62

Qy         71 FISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPFRL 130
              |: |||||  ||     || |||: |:|       | ||| || ||| :|| ||||:|||||
Db         63 FVFTLPFRI-YYFVVRNWPFGDVLCKISVTLFYTNMYGSILFLTCISVDRFLAIVHPFRS 121

Qy        131 LHVTSIRSAWILCGIIWILIMASSI---MLLDSGSEQNGSVTSCLELNLYKIAKLQTMNY 187
                : : |:| |:| :|| ::| |            : : |      :| | |  :       ::
Db        122 KTLRTKRNARIVCVAVWITVLAGSTPASFFQSTNRQNNTEQRTCFE-NFPESTWKTYLSR 180

Qy        188 IAL---VVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCF 244
              | :    :|| :|        | :::| | |  :  |  ::| :| :| |  | :| :||  ||
Db        181 IVIFIEIVGFFIPLILNVTCSTMVLRTLNK-PLTLSRNKLSKKKVLKMIFVHLVIFCFCF 239

Qy        245 LPYH-------TLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGE 294
              :||:           :||    ||               :      :|| :| :| ||:|::||| :
Db        240 VPYNITLILYSLMRT---QTWINCSVVTAVRTMYPVTLCIAVSNCCFDPIVYYFTSD 293
```

RESULT 3
JC4737
G protein-coupled receptor P2Y1 - human
N;Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor
C;Species: Homo sapiens (man)
C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 17-Nov-2000
C;Accession: JC4737; JC4615; S54253
R;Janssens, R.; Communi, D.; Pirotton, S.; Samson, M.; Parmentier, M.; Boeynaems, J.M.
Biochem. Biophys. Res. Commun. 221, 588-593, 1996
A;Title: Cloning and tissue distribution of the human P2Y1 receptor.
A;Reference number: JC4737; MUID:96205320; PMID:8630005
A;Accession: JC4737
A;Molecule type: DNA
A;Residues: 1-373 <JAN>
A;Cross-references: GB:S81950; NID:g1839438; PIDN:AAB47091.1; PID:g1839439
R;Ayyanathan, K.; Webbs, T.E.; Sandhu, A.K.; Athwal, R.S.; Barnard, E.A.; Kunapuli, S
Biochem. Biophys. Res. Commun. 218, 783-788, 1996
A;Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor.
A;Reference number: JC4615; MUID:96158962; PMID:8579591
A;Accession: JC4615
A;Molecule type: mRNA
A;Residues: 1-373 <AYY>
A;Cross-references: GB:U42029; NID:g1147730; PIDN:AAA97872.1; PID:g1147731
A;Experimental source: erythro leukemia cells
R;Leon, C.; Vial, C.; Cazenave, J.; Gachet, C.
submitted to the EMBL Data Library, May 1995
A;Description: Cloning of a human putative P2Y receptor.
A;Reference number: S54253
A;Accession: S54253
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-137,139-373 <LEO>
A;Cross-references: EMBL:Z49205; NID:g798835; PIDN:CAA89066.1; PID:g798836
C;Comment: This receptor belongs to a family of G protein-coupled receptors. It respc
C;Genetics:
A;Gene: p2Y1; GDB:P2RY1
A;Cross-references: GDB:677125; OMIM:601167
A;Map position: 3pter-3qter
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p
F;52-77/Domain: transmembrane #status predicted <TM1>
F;88-111/Domain: transmembrane #status predicted <TM2>
F;124-152/Domain: transmembrane #status predicted <TM3>
F;171-191/Domain: transmembrane #status predicted <TM4>
F;214-237/Domain: transmembrane #status predicted <TM5>
F;261-282/Domain: transmembrane #status predicted <TM6>
F;305-328/Domain: transmembrane #status predicted <TM7>
F;11,27,113,197/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;258,336/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status pred
F;330,339/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status pred
F;343/Binding site: phosphate (Ser) (covalent) (by protein kinase C and calmodulin-de

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  Query Match             26.1%;  Score 446;  DB 2;  Length 373;
  Best Local Similarity   32.1%;  Pred. No. 7.5e-30;
  Matches  102;  Conservative   79;  Mismatches  111;  Indels   26;  Gaps   10;

Qy          6 TFSNNNSRNC--TIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLN 63
              | : ::|  |   |    |:   :  | ||:::|  | ||| ::|::|:    |   : ::|:| |
Db         33 TAAVSSSFKCALTKTGFQFYYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFN 92

Qy         64 LAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLA 123
              ||::| |:: |||      ||        :::||||  |::  :  ::||::| || ||| :| |:
Db         93 LALADFLYVLTLPALIFYYFNKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSG 152

Qy        124 MVHPFRLLHVTSIRSAWILCGIIW-ILIMASSIMLLDSGS--EQNGSVTSCLE------L 174
              :|:| : |       ::|   :  ::| |:::| | :|  ||:    :| ::| | :          |
Db        153 VVYPLKSLGRLKKKNAICISVLVWLIVVVAISPILFYSGTGVRKNKTIT-CYDTTSDEYL 211

Qy        175 NLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTII 234
                | |  :  |       : : | :|    :  || ||:| |:  ::   | ||    ||:: :|
Db        212 RSYFIYSMCT----TVAMFC-VPLVLILGCYGLIVRALIYKDLDNSPLR---RKSIYLVI 263

Qy        235 ITLIIFFLCFLPYHTLRTVHLTT----WKVGLC--KDRLHKALVITLALAAANACFNPLL 288
              | |  :| :  ::|:| ::|::|                 :|     ||::     :|   ||: |:| :|:|
Db        264 IVLTVFAVSYIPFHVMKTMNLRARLDFQTPAMCAFNDRVYATYQVTRGLASLNSCVDPIL 323

Qy        289 YYFAGENFKDRLKSALRK 306
              |: ||: |: ||  | ||
Db        324 YFLAGDTFRRRLSRATRK 341
```

RESULT 4
JC4162
P2Y receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 12-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 24-Sep-1999
C;Accession: JC4162
R;Henderson, D.J.; Elliot, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.

```
Biochem. Biophys. Res. Commun. 212, 648-656, 1995
A;Title: Cloning and characterisation of a bovine P2Y receptor.
A;Reference number: JC4162; MUID:95352058; PMID:7626079
A;Accession: JC4162
A;Molecule type: mRNA
A;Residues: 1-373 <HEN>
A;Cross-references: EMBL:X87628; NID:g1032484; PIDN:CAA60958.1; PID:g1032485
A;Experimental source: aortic endothelial cell
C;Genetics:
A;Gene: bovp2y
C;Superfamily: ATP receptor P2u
C;Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
F;52-77/Domain: transmembrane #status predicted <TM1>
F;88-111/Domain: transmembrane #status predicted <TM2>
F;124-150/Domain: transmembrane #status predicted <TM3>
F;171-191/Domain: transmembrane #status predicted <TM4>
F;214-237/Domain: transmembrane #status predicted <TM5>
F;261-282/Domain: transmembrane #status predicted <TM6>
F;305-328/Domain: transmembrane #status predicted <TM7>
F;11,27,113,197/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;258/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

  Query Match             25.8%;  Score 442;  DB 2;  Length 373;
  Best Local Similarity   31.0%;  Pred. No. 1.6e-29;
  Matches   95;  Conservative   78;  Mismatches  109;  Indels   24;  Gaps    7;

Qy         16 TIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLLFISTL 75
                |   |:  :  | ||:::|  | |||  ::|::|:     |   :  ::|:|  |||::|  |:: ||
Db         45 TKTGFQFYYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTL 104

Qy         76 PFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPFRLLHVTS 135
                |     ||    ::|||||   |::   :   :||:|  || |||  :|   |:   :|:|  :  |
Db        105 PALIFYYFNKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLK 164

Qy        136 IRSAWILCGIIWILIMASSIMLL---DSGSEQNGSVTSCLE------LNLYKIAKLQTMN 186
                ::|  :   ::|::::      :|      :|    :|   ::|  | :           |   |   |    :  |
Db        165 KKNAVYISVLVWLIVVVGISPILFYSGTGIRKNKTIT-CYDTTSDEYLRSYFIYSMCT-- 221

Qy        187 YIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFLP 246
                  :  :  |  :|    :   ||  ||:|  |:   ::    |  ||      ||::   :||  |  :|  :  ::|
Db        222 --TVAMFC-VPLVLILGCYGLIVRALIYKDLDNSPLR---RKSIYLVIIVLTVFAVSYIP 275

Qy        247 YHTLRTVHL------TTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
                :|  ::|::|          |  ::       ||::        :|    ||:  |:|  :|:||:  ||:  |:  ||
Db        276 FHVMKTMNLRARLDFQTPEMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335

Qy        301 KSALRK 306
                  |  ||
Db        336 SRATRK 341


RESULT 5
B45680
G protein-coupled peptide receptor EBI 2 - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: B45680
R;Birkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A;Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled p
A;Reference number: A45680; MUID:93188173; PMID:8383238
A;Accession: B45680
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-361 <BIR>
A;Cross-references: GB:L08177; NID:g292056; PIDN:AAA35924.1; PID:g292057
A;Experimental source: B-lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:127096, NCBIP:127097)
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match             25.7%;  Score 440;  DB 2;  Length 361;
  Best Local Similarity   32.1%;  Pred. No. 2.3e-29;
  Matches  102;  Conservative   63;  Mismatches  135;  Indels   18;  Gaps    7;

Qy          3 PNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFML 62
                |: |     |:           :   |      |:  |  ::|     |::||  |::  |  :|     ||   |     ::
Db         12 PSATPQGNDCDLYAHHSTARIVMPLHYSLVFIIGLVGNLLALVVIVQNRKKINSTTLYST 71

Qy         63 NLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFL 122
                || |||:||  :  ||  |    ||     |  :|     ||     |||  :       :|  |:  :  |:|  ||:  ||:
Db         72 NLVISDILFTTALPTRIAYYAMGFDWRIGDALCRITALVFYINTYAGVNFMTCLSIDRFI 131

Qy        123 AMVHPFRLLHVTSIRSAWILCGIIWILIMASSI-MLLDSGSEQNGSVTSCLEL-NLYKIA 180
                |:|||  |      :    |     |    :|    :|||:  |  ::  :|::    |:|         :|:|    |     :
Db        132 AVVHPLRYNKIKRIEHAKGVCIFVWILVFAQTLPLLINPMSKQEAERITCMEYPNFEETK 191

Qy        181 KLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVE-----VPESGLRVSHRKALTTIII 235
                  |    :       |    :|  :||      :  |||      |          |    :                :||:      ::|||  |||:
Db        192 SLPWILLGACFIGYVLPLIIILICYSQICCKLFRTAKQNPLTEKSGV---NKKALNTIIL 248

Qy        236 TLIIFFLCFLPYHTLRTVHLTTWKVGL-----CKDR--LHKALVITLALAAANACFNPLL 288
                :::|  |||  |||          |:          |:                   |        |           :|       |:  |          |  |  :|  :
Db        249 IIVVFVLCFTPYHVAIIQHMIK-KLRFSNFLECSQRHSFQISLHFTVCLMNFNCCMDPFI 307

Qy        289 YYFAGENFKDRLKSALRK 306
                |:||   :  :|  ::      |::
Db        308 YFFACKGYKRKVMRMLKR 325


RESULT 6
T09508
intron 17 purinergic receptor P2Y5 - human
N;Alternate names: G-protein coupled receptor
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999
C;Accession: T09508
R;Bohm, S.K.; Trumpp, A.; Khitin, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W.
submitted to the EMBL Data Library, April 1997
A;Description: The human purinergic receptor P2Y5 is encoded in intron 17 of the ret
A;Reference number: Z16705
A;Accession: T09508
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-344 <BOH>
A;Cross-references: EMBL:AF000546; NID:g2232068; PID:g2232069
C;Genetics:
A;Map position: 13
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match             25.5%;  Score 436;  DB 2;  Length 344;
  Best Local Similarity   32.0%;  Pred. No. 4.7e-29;
  Matches   98;  Conservative   73;  Mismatches  113;  Indels   22;  Gaps    8;

Qy         11 NSRNCTI-ENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDL 69
                || :|     ::||     :     :: ::|    |::  |  ::||:|:      |                :|:|||:|||
Db          5 NSSHCFYNDSFKYTLYGCMFSMVFVLGLVSNCVAIYIFICVLKVRNETTTYMINLAMSDL 64

Qy         70 LFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPFR 129
                ||: |||||    :|        ||  ||||  |:|          |  |||  ||  |||  :||  ||||:|:|||:
Db         65 LFVFTLPFRI-FYFTTRNWPFGDLLCKISVMLFYTNMYGSILFLTCISVDRFLAIVYPFK 123

Qy        130 LLHVTSIRSAWILCGIIWILIM---ASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQTMN 186
                  :  :  |:|  |:|   :|:  ::      |  ::  :     :  |:  |    :|  |    |     :            ::
Db        124 SKTLRTKRNAKIVCTGVWLTVIGGSAPAVFVQSTHSQGNNASEACFE-NFPEATWKTYLS 182

Qy        187 YIAL---VVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLC 243
                  |  :      :||   :|          |   ::::  |   |    |     |     :::     |   |      |  :  ||||    |
Db        183 RIVIFIEIVGFFIPLILNVTCSSMVLKTLTK-PVTLSRSKINKTKVLKMIFVHLIIFCFC 241

Qy        244 FLPYHTLRTVHLTTWKVGLCKDRLHKALV--------ITLALAAANACFNPLLYYFAGEN 295
                |:||:        ::|    :  :      :   ::  ::|                |||  :|  :|  ||:|::|||    :
Db        242 FVPYN----INLILYSLVRTQTFVNCSVVAAVRTMYPITLCIAVSNCCFDPIVYYFTSDT 297

Qy        296 FKDRLK 301
```

```
              :: :|
Db        298 IQNSIK 303
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RESULT 7
JC5549
heptahelical P2Y5-like receptor - human
C;Species: Homo sapiens (man)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 24-Sep-1999
C;Accession: JC5549
R;Janssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D.
Biochem. Biophys. Res. Commun. 236, 106-112, 1997
A;Title: Cloning of a human heptahelical receptor closely related to the P2Y5 receptor.
A;Reference number: JC5549; MUID:97366605; PMID:9223435
A;Accession: JC5549
A;Molecule type: DNA
A;Residues: 1-370 <JAN>
A;Cross-references: DDBJ:AF005419; NID:g2240034; PIDN:AAB66322.1; PID:g2240035
C;Superfamily: ATP receptor P2u

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  Query Match             25.1%;  Score 430;  DB 2;  Length 370;
  Best Local Similarity   31.7%;  Pred. No. 1.6e-28;
  Matches  103;  Conservative   70;  Mismatches  132;  Indels   20;  Gaps    9;

Qy          5 GTFSNNNSRNCTI-ENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLN 63
                |  : ||:  | : ::||      || ::|  |:: | :|::||    |  :    :|: |
Db         23 GNATANNT--CIVDDSFKYNLNGAVYSVVFILGLITNSVSLFVFCFRMKMRSETAIFITN 80

Qy         64 LAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLA 123
              ||:|||||: ||||:  :|     :| |||  |:|    :   |:| |: ||| :|| ||||
Db         81 LAVSDLLFVCTLPFKI-FYNFNRHWPFGDTLCKISGTAFLTNIYGSMLFLTCISVDRFLA 139

Qy        124 MVHPFRLLHVTSIRSAWILCGIIWILIMASSIML-LDSGSEQNGSVTSCLELNLYKIAK- 181
              :|:|||    : : |:: |:|   :|||:::   |     |  |  :   | : |:|  |     :: |
Db        140 IVYPFRSRTIRTRRNSAIVCAGVWILVLSGGISASLFSTTNVNNATTTCFEGLSKRVWKT 199

Qy        182 -LQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIF 240
               |  :      ||| ::|       |  :::| | |     | :   : :| |   | : : :|
Db        200 YLSKITIFIEVVGFIIPLILNVSCSSVVLRTLRK-PATLSQIGTNKKKVLKMITVHMAVF 258

Qy        241 FLCFLPYHTLRTVHLTTWKVGLCK---DRLHKALV-ITLALAAANACFNPLLYYFAGENF 296
              :||:||:::  ::       :       :|   | :  ||| ||   | ||:| :||| |:|
Db        259 VVCFVPYNSVLFLYALVRSQAITNCFLERFAKIMYPITLCLATLNCCFDPFIYYFTLESF 318

Qy        297 KD--------RLKSALRKGHPQKAK 313
              :         |::|  :   |   |
Db        319 QKSFYINAHIRMESLFKTETPLTTK 343
```

RESULT 8
A47556
ATP receptor P2u - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C;Accession: A47556
R;Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993
A;Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells.
A;Reference number: A47556; MUID:93281707; PMID:7685114
A;Accession: A47556
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-373 <LUS>
A;Cross-references: GB:L14751; NID:g309457; PIDN:AAA39871.1; PID:g309458
C;Superfamily: ATP receptor P2u
C;Keywords: transmembrane protein

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  Query Match             24.4%;  Score 418.5;  DB 2;  Length 373;
  Best Local Similarity   31.8%;  Pred. No. 1.5e-27;
  Matches  106;  Conservative   67;  Mismatches  131;  Indels   29;  Gaps   10;

Qy          1 MEP-----NGTFSNNN-SRNCTI-ENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKK 53
               :||      |||:  :      |   |:||    |: | ::    |:  | :::|:||    |

Db          5 LEPWNSTINGTWEGDELGYKCRFNEDFKYVLLPVSYGVVCVLGLCLNVVALYIFLCRLKT 64

Qy         54 STSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFL 113
              :   :| :||:|| |: ::||      || || :| |   : |::: :   | |:| || ||
Db         65 WNASTTYMFHLAVSDSLYAASLPLLVYYYARGDHWPFSTVLCKLVRFLFYTNLYCSILFL 124

Qy        114 TVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIML------DSGSEQNGS 167
              | :|| | | :: |     |       | |  :  ::|:|::|      :|          |:
Db        125 TCISVHRCLGVLRPLHSLRWGRARYARRVAAVVWVLVLACQAPVLYFVTTSVRGTRITCH 184

Qy        168 VTSCLELNLYKIAKLQTMNYIALVVGCL--LPFFTLSICYLLIIRVLLKVEV-PESGLRV 224
              ||  ||  : :|         | :::|  |  :||  : :||:|: | |||            ||
Db        185 DTSARELFSHFVA------YSSVMLGLLFAVPFSVILVCYVLMARRLLKPAYGTTGGLPR 238

Qy        225 SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGL-CK--DRLHKALVITLALAAAN 281
              : ||:: || :  | :| ||||:|  ||::  :     : |  |    : :: |    ||  ||:||
Db        239 AKRKSVRTIALVLAVFALCFLPFHVTRTLYYSFRSLDLSCHTLNAINMAYKITRPLASAN 298

Qy        282 ACFNPLLYYFAGENFKDRLKSALRKGHPQKAKT 314
              :| :|:||: ||:       ||      |      |      |
Db        299 SCLDPVLYFLAGQ----RLVRFARDAKPPTEPT 327
```

RESULT 9
S13638
platelet-activating factor receptor - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 08-Oct-1999
C;Accession: S13638
R;Honda, Z.; Nakamura, M.; Miki, I.; Minami, M.; Watanabe, T.; Seyama, Y.; Okado, H.,
Nature 349, 342-346, 1991
A;Title: Cloning by functional expression of platelet-activating factor receptor from
A;Reference number: S13638; MUID:91101726; PMID:1846231
A;Accession: S13638
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-342 <HON>
A;Cross-references: GB:X56736; NID:g49442; PIDN:CAA40060.1; PID:g49443
A;Note: the species of guinea pig is not identified; in GenBank entry CCPAFREC, relea
C;Superfamily: ATP receptor P2u

```
  Query Match             24.3%;  Score 416;  DB 2;  Length 342;
  Best Local Similarity   30.4%;  Pred. No. 2.2e-27;
  Matches   97;  Conservative   67;  Mismatches  137;  Indels   18;  Gaps    7;

Qy         11 NSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVF--LQPYKKSTSVNVFMLNLAISD 68
              || :        |:    ||||| |||  |:: ||  ::||   | | ||       : :||:|| ::|
Db          4 NSSSRVDSEFRYTLFPIVYSIIFVLGIIANGYVLWVFARLYPSKKLNEIKIFMVNLTVAD 63

Qy         69 LLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPF 128
              |||: |||      ||      ||          | :        ::| | |: || |:: || |: :|
Db         64 LLFLITLPLWIVYYSNQGNWFLPKFLCNLAGCLFFINTYCSVAFLGVITYNRFQAVKYPI 123

Qy        129 RLLHVTSIRSAWILCGIIWILIM--ASSIMLLD-----SGSEQNGSVTSCLELNLYKIAK 181
              :     |: :      |  :||: |:  ||  :::|       |       :|::| | | :   | :|
Db        124 KTAQATTRKRGIALSLVIWVAIVAAASYFLVMDSTNVVSNKAGSGNITRCFF-HYEKGSK 182

Qy        182 LQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFF 241
                : :| :|:|  : |    :  | |:|| ||: | :               |:|| :    | :|
Db        183 PVLIIHICIVLGFFIVFLLILFCNLVIIHTLLRQPVKQQRNAEVRRRALWMVCTVLAVFV 242

Qy        242 LCFLPYHTLRTVHLTTWKVGLCKDRLHKAL----VITLALAAANACFNPLLYYFAGENFK 297
              :||:|:|  :: :  |   ::|:       |:|:       :||  | : |      :|::| |   : |:
Db        243 ICFVPHHMVQ-LPWTLAELGMWPSSNHQAINDAHQVTLCLLSTNCVLDPVIYCFLTKKFR 301

Qy        298 DRLKSALRKGHPQKAKTKC 316
                |    |    :  ::  ||
Db        302 KHLSEKL---NIMRSSQKC 317
```

RESULT 10
A54946
P-2U nucleotide receptor - human

C;Species: Homo sapiens (man)
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 17-Mar-1999
C;Accession: A54946
R;Parr, C.E.; Sullivan, D.M.; Paradiso, A.M.; Lazarowski, E.R.; Burch, L.H.; Olsen, J.C.
Proc. Natl. Acad. Sci. U.S.A. 91, 3275-3279, 1994
A;Title: Cloning and expression of a human P-2U nucleotide receptor, a target for cystic
A;Reference number: A54946; MUID:94211846; PMID:8159738
A;Accession: A54946
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-375 <PAR>
A;Cross-references: GB:U07225
A;Note: parts of this sequence were confirmed by protein sequencing
C;Genetics:
A;Gene: GDB:P2RY2; HP2U; P2U
A;Cross-references: GDB:362713; OMIM:600041
A;Map position: 11q13.5-11q14.1
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein

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  Query Match             24.3%;  Score 416;  DB 2;  Length 375;
  Best Local Similarity   31.6%;  Pred. No. 2.4e-27;
  Matches  100;  Conservative   67;  Mismatches  131;  Indels   18;  Gaps    8;

Qy          4 NGTFSNNN-SRNCTI-ENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFM 61
                |||:  :     |   |:||    |: | ::   |:  | : :|:||   |   :   :|
Db         13 NGTWDGDELGYRCRFNEDFKYVLLPVSYGVVCVLGLCLNAVGLYIFLCRLKTWNASTTYM 72

Qy         62 LNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRF 121
                :||:|| |: ::||     || || :| |   : |::: :   | |:| || ||| :|| |
Db         73 FHLAVSDALYAASLPLLVYYYARGDHWPFSTVLCKLVRFLFYTNLYCSILFLTCISVHRC 132

Qy        122 LAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK 181
              | :: | | |     | |   : | :|:|::|      :|    :           :| :  :  ::
Db        133 LGVLRPLRSLRWGRARYARRVAGAVWVLVLACQAPVLYFVTTSARGPLTCHDTSAPELFS 192

Qy        182 LQTMNYIALVVGCL--LPFFTLSICYLLIIRVLLKVEVPES-GLRVSHRKALTTIIITLI 238
               : : | ::::| |  :|   : :||:|: | |||      | ||    : ||:: || : |
Db        193 -RFVAYSSVMLGLLFAVPFFAVILVCYVLMARRLLKPAYGTSGGLPRAKRKSVRTIAVVLA 251

Qy        239 IFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLA-----LAAANACFNPLLYYFAG 293
              :| |||||:|  ||:: :    : |      |      | :|          ||:||:| :|:||: ||
Db        252 VFALCFLPFHVTRTLYYSFRSLDL---SCHTLNAINMAYKVTRLASANSCLDPVLYFLAG 308

Qy        294 ENFKDRLKSALRKGHP 309
              :    ||   |  |
Db        309 Q----RLVRFARDAKP 320
```

RESULT 11
A40191
platelet-activating factor receptor - human
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 20-Jun-2000
C;Accession: A40191; JH0479; A41079; JC1359; A42831; I51923
R;Kunz, D.; Gerard, N.P.; Gerard, C.
J. Biol. Chem. 267, 9101-9106, 1992
A;Title: The human leukocyte platelet-activating factor receptor. cDNA cloning, cell sur
A;Reference number: A40191; MUID:92250505; PMID:1374385
A;Accession: A40191
A;Molecule type: mRNA
A;Residues: 1-342 <KUN>
A;Cross-references: GB:M76674; NID:g456293; PIDN:AAA60002.1; PID:g456294
R;Ye, R.D.; Prossnitz, E.R.; Zou, A.; Cochrane, C.G.
Biochem. Biophys. Res. Commun. 180, 105-111, 1991
A;Title: Characterization of a human cDNA that encodes a functional receptor for platele
A;Reference number: JH0479; MUID:92028922; PMID:1656963
A;Accession: JH0479
A;Molecule type: mRNA
A;Residues: 1-342 <YER>
A;Cross-references: GB:M80436; NID:g189537; PIDN:AAA60001.1; PID:g189538
A;Experimental source: granulocyte, cell line HL-60 all
R;Nakamura, M.; Honda, Z.; Izumi, T.; Sakanaka; C.; Mutoh, H.; Minami, M.; Bito, H.; Sey
J. Biol. Chem. 266, 20400-20405, 1991
A;Title: Molecular cloning and expression of platelet-activating factor receptor fro
A;Reference number: A41079; MUID:92041873; PMID:1657923
A;Accession: A41079
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-342 <NAK>
A;Cross-references: GB:D10202; GB:D90433; NID:g219975; PIDN:BAA01050.1; PID:g219976
R;Sugimoto, T.; Tsuchimochi, H.; McGregor, C.G.A.; Mutoh, H.; Shimizu, T.; Kurachi,
Biochem. Biophys. Res. Commun. 189, 617-624, 1992
A;Title: Molecular cloning and characterization of the platelet-activating factor re
A;Reference number: JC1359; MUID:93112021; PMID:1281995
A;Accession: JC1359
A;Molecule type: mRNA
A;Residues: 1-315,'N',317-342 <SUG>
A;Experimental source: heart
A;Note: the authors translated the codon AAT for residue 316 as Lys
R;Seyfried, C.E.; Schweickart, V.L.; Godiska, R.; Gray, P.W.
Genomics 13, 832-834, 1992
A;Title: The human platelet-activating factor receptor gene (PTAFR) contains no intr
A;Reference number: A42831; MUID:92347886; PMID:1322356
A;Accession: A42831
A;Molecule type: DNA
A;Residues: 1-226,'TG',229-342 <SEY>
A;Cross-references: GB:M88177; NID:g190697; PIDN:AAA60214.1; PID:g190698
A;Note: sequence extracted from NCBI backbone (NCBIN:109813, NCBIP:109814)
R;Chase, P.B.; Halonen, M.; Regan, J.W.
Am. J. Respir. Cell Mol. Biol. 8, 240-244, 1993
A;Title: Cloning of a human platelet-activating factor receptor gene: evidence for a
A;Reference number: I51923; MUID:93192035; PMID:8383507
A;Accession: I51923
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-342 <RES>
A;Cross-references: GB:S56396; NID:g298580; PIDN:AAB25755.1; PID:g298581
C;Genetics:
A;Gene: GDB:PTAFR
A;Cross-references: GDB:128806; OMIM:173393
A;Map position: 1p35-1p34.3
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
F;17-38/Domain: transmembrane #status predicted <TRI>
F;54-75/Domain: transmembrane #status predicted <TII>
F;92-113/Domain: transmembrane #status predicted <III>
F;134-155/Domain: transmembrane #status predicted <TIV>
F;184-205/Domain: transmembrane #status predicted <TRV>
F;233-253/Domain: transmembrane #status predicted <TVI>
F;277-297/Domain: transmembrane #status predicted <VII>

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  Matches  103;  Conservative   64;  Mismatches  137;  Indels   25;  Gaps    9;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVF--LQPYKKSTSVN 58
              |||: : |: :|        |:  ||||| ||| ||: ||  ::|| | | ||   :
Db          1 MEPHDS-SHMDS------EFRYTLFPIVYSIIFVLGVIANGYVLWVFARLYPCKKFNEIK 53

Qy         59 VFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSV 118
              :||:|| ::|:||: |||     ||      |||       | :       ::| | |: || |::
Db         54 IFMVNLTMADMLFLITLPLWIVYYQNQGNWILPKFLCNVAGCLFFINTYCSVAFLGVITY 113

Qy        119 VRFLAMVHPFRLLHVTSIRSAWILCGIIWILIM--ASSIMLLDS-----GSEQNGSVTSC 171
              || |:  | :       : :    | :||: |: ||  ::|||      |  :|:|| |
Db        114 NRFQAVTRPIKTAQANTRKRGISLSLVIWVAIVGAASYFLILDSTNTVPDSAGSGNVTRC 173

Qy        172 LELNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALT 231
              | :   | :      : :| :|    | |  :  { |:|||  ||    | :         |:||
Db        174 FE-HYEKGSVPVLIIHIFIVFSFFLVFLIILFCNLVIIRTLLMQPVQQQRNAEVKRRALW 232

Qy        232 TIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKAL----VITLALAAANACFNPL 287
               :    | :| :||:|:| :: :  |   ::|     : |:|:       :|| | : |    :|:
Db        233 MVCTVLAVFIICFVPHHVVQ-LPWTLAELGFQDSKFHQAINDAHQVTLCLLSTNCVLDPV 291
```

```
Qy        288 LYYFAGENFKDRLKSALRKGHPQKAKTKC 316
              :| |  : |:   |     | :  ::  ||
Db        292 IYCFLTKKFR---KHLTEKFYSMRSSRKC 317
```

RESULT 12
I51667
thrombin receptor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I51667
R;Gerszten, R.E.; Chen, J.; Ishii, M.; Ishii, K.; Nanevicz, T.; Turck, C.W.; Vu, T.H.; C
Nature 368, 648-651, 1994
A;Title: Thrombin receptor's specificity for agonist peptide is determined by its extrac
A;Reference number: I51667; MUID:94195429; PMID:8145852
A;Accession: I51667
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-420 <GER>
A;Cross-references: EMBL:U09632; NID:g495197; PIDN:AAA18498.1; PID:g495198

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  Query Match            23.6%;  Score 404.5;  DB 2;  Length 420;
  Best Local Similarity  32.4%;  Pred. No. 2.5e-26;
  Matches   99;  Conservative   61;  Mismatches  123;  Indels   23;  Gaps    6;

Qy         13 RNCTIE-------NFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA 65
              || | |          :  :| | :| ::|  |:  | |:| :||   |        |:|||||
Db         85 RNITKEAEQYLSSQWLTKFVPSLYTVVFIVGLPLNLLAIIIFLFKMKVRKPAVVYMLNLA 144

Qy         66 ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMV 125
              |:|: |:| |||:  |:| |::|:||  |||::   | |||  |:  :  :|| ||||:|
Db        145 IADVFFVSVLPFKIAYHLSGNDWLFGPGMCRIVTAIFYCNMYCSVLLIASISVDRFLAVV 204

Qy        126 HPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQ---NGSVTSCLELNLYKIAKL 182
              :|   |    ::  |::  | ||:: :||:| || :   |        :|:| ::   |  |
Db        205 YPMHSLSWRTMSRAYMACSFIWLISIASTIPLLVTEQTQKIPRLDITTCHDVLDLKDLKD 264

Qy        183 QTMNYIALVVGCLL----PFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLI 238
               : | :    |||    ||   :|||: ||| |    :  |        :||    :: |
Db        265 FYIYYFSSF--CLLFFFVPFIITTICYIGIIRSLSSSIENS---CKKTRALFLAVVVLC 319

Qy        239 IFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKD 298
              :| :|| | : |      |        :        : |: | :::  : : : | :||:||:|     :
Db        320 VFIICFGPTNVLFLTHY----LQEANEFLYFAYILSACVGSVSCCLDPLIYYYASSQCQR 375

Qy        299 RLKSAL 304
               | | |
Db        376 YLYSLL 381
```

RESULT 13
S63666
platelet activating factor receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Accession: S63666
R;Ishii, S.; Matsuda, Y.; Nakamura, M.; Waga, I.; Kume, K.; Izumi, T.; Shimizu, T.
Biochem. J. 314, 671-678, 1996
A;Title: A murine platelet-activating factor receptor gene: cloning, chromosomal localiz
A;Reference number: S63666; MUID:96239129; PMID:8670084
A;Accession: S63666
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-341 <ISH>
A;Cross-references: EMBL:D50872; NID:g1256924; PIDN:BAA09468.1; PID:g1256925
C;Superfamily: ATP receptor P2u

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  Query Match            23.6%;  Score 404;  DB 2;  Length 341;
  Best Local Similarity  30.5%;  Pred. No. 2.2e-26;
  Matches  101;  Conservative   66;  Mismatches  134;  Indels   30;  Gaps   10;

Qy          1 MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVF--LQPYKKSTSVN 58
              || ||:|  ::          |:   ||||| :||  ||: ||   ::||  | | ||   :
Db          1 MEHNGSFRVDS-------EFRYTLFPIVYSVIFILGVVANGYVLWVFANLYPSKKLNEIK 53

Qy         59 VFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSV 118
              :||:|| ::||||: |||    ||     :||  :  | :      ::| | |: || |::
Db         54 IFMVNLTMADLLFLITLPLWIVYYYNEGDWILPNFLCNVAGCLFFINTYCSVAFLGVITY 113

Qy        119 VRFLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGS-------EQNGSVTSC 171
               |: |: :| :      |: :    |  |||: |:|::    | : |          : :|::| |
Db        114 NRYQAVAYPIKTAQATTRKRGISLSLIIWVSIVATASYFLATDSTNLVPNKDGSGNITRC 173

Qy        172 LE-LNLYKIAKLQTMNYIALVVGC-LLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKA 229
                |      | :  |      :||      |  | ||  :  | |:||  ||     :  :        |:|
Db        174 FEHYEPYSVPILVVHVFIAF---CFFLVFFLIFYCNLVIIHTLLTQPMRQQRKAGVKRRA 230

Qy        230 LTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKAL----VITLALAAANACFN 285
               |   :     | :|  :||:|:| :: :   |    ::|   :   |:|:       ||| |  :  |     :
Db        231 LWMVCTVLAVFIICFVPHHVVQ-LPWTLAELGY-QTNFHQAINDAHQITLCLLSTNCVLD 288

Qy        286 PLLYYFAGENFKDRLKSALRKGHPQKAKTKC 316
              |::| |   : |:   |        | :   ::  ||
Db        289 PVIYCFLTKKFRKHLS---EKFYSMRSSRKC 316
```

RESULT 14
S66518
proteinase-activated receptor 2 precursor - human
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000
C;Accession: S66518; S64709; G02131
R;Nystedt, S.; Emilsson, K.; Larsson, A.K.; Stroembeck, B.; Sundelin, J.
Eur. J. Biochem. 232, 84-89, 1995
A;Title: Molecular cloning and functional expression of the gene encoding the human p
A;Reference number: S66518; MUID:96048032; PMID:7556175
A;Accession: S66518
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-397 <NYS>
A;Cross-references: EMBL:Z49993; NID:g1008084; PIDN:CAA90290.1; PID:g1008085
R;Boehm, S.K.; Kong, W.; Broemme, D.; Smeekens, S.P.; Anderson, D.C.; Connolly, A.; K
Biochem. J. 314, 1009-1016, 1996
A;Title: Molecular cloning, expression and potential functions of the human proteinas
A;Reference number: S64709; MUID:96177879; PMID:8615752
A;Accession: S64709
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-137,'A',139-397 <BOE>
A;Cross-references: EMBL:U34038; NID:g1041728; PIDN:AAB47871.1; PID:g1041729
A;Note: the authors translated the codon GTC for residue 68 as Ile and AAC for residu
R;Kahn, M.L.; Coughlin, S.R.
submitted to the EMBL Data Library, September 1995
A;Reference number: H00822
A;Accession: G02131
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 29-397 <KAH>
A;Cross-references: EMBL:U36753; NID:g1208539; PIDN:AAA90957.1; PID:g1208540
C;Genetics:
A;Map position: 5q13
A;Introns: 28/1
C;Superfamily: ATP receptor P2u
F;1-36/Domain: activation peptide #status predicted <APT>
F;1-25/Domain: signal sequence #status predicted <SIG>
F;37-397/Product: proteinase-activated receptor 2 #status predicted <MAT>

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  Query Match            23.4%;  Score 400.5;  DB 2;  Length 397;
  Best Local Similarity  30.7%;  Pred. No. 5.1e-26;
  Matches   99;  Conservative   69;  Mismatches  121;  Indels   33;  Gaps    9;

Qy         24 FFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLLFISTLPFRADYYL 83
               | |||| |:|  |:  ||::::|||  ||     ::| |||::|||  :   |  :  |::
Db         77 FLPIVYTIVFVVGLPSNGMALWVFLFRTKKKHPAVIYMANLALADLLSVIWFPLKIAYHI 136

Qy         84 RGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILC 143
```

```
              |:|||:|:  | ::    | ||| || |:| ||| |:  :|:|       | : | |
Db        137 HGNNWIYGEALCNVLIGFFYGNMYCSILFMTCLSVQRYWVIVNPMG----HSRKKANIAI 192

Qy        144 GI---IWILIMASSIML-----------LDSGSEQNGSVTSCLELNLYKIAKLQTMNY-I 188
              ||   ||:||:  :| |           |          ::|:| ::   ::      || :
Db        193 GISLAIWLLILLVTIPLYVVKQTIFIPAL--------NITTCHDVLPEQLLVGDMFNYFL 244

Qy        189 ALVVGC-LLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFLPY 247
               :| :|  | | |  :  |:|:||:|     : |:  :     ::|:  |:  | :: :|| |
Db        245 SLAIGVFLFPAFLTASAYVLMIRMLRSSAMDENSEK-KRKRAIKLIVTVLAMYLICFTPS 303

Qy        248 HTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRLKSALRKG 307
               : |  ||    |     :  ::    :: | |:  |:| :| :|||    :|:|  |:||
Db        304 NLLLVVHYFLIK-SQGQSHVYALYIVALCLSTLNSCIDPFVYYFVSHDFRDHAKNALL-- 360

Qy        308 HPQKAKTKCVFPVSVWLRKETR 329
                :  :|      ||:  :| :|
Db        361 -CRSVRTVKQMQVSLTSKKHSR 381
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RESULT 15
I38435
angiotensin receptor homolog APJ - human
C;Species: Homo sapiens (man)
C;Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 21-Jul-2000
C;Accession: I38435
R;O'Dowd, B.F.; Heiber, M.; Chan, A.; Heng, H.H.; Tsui, L.; Kennedy, J.L.; Shi, X.; Petr
Gene 136, 355-360, 1993
A;Title: A human gene that shows identity with the gene encoding the angiotensin recepto
A;Reference number: I38435; MUID:94124031; PMID:8294032
A;Accession: I38435
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-380 <RES>
A;Cross-references: EMBL:U03642; NID:g425351; PIDN:AAA18954.1; PID:g425352
C;Genetics:
A;Gene: APJ
A;Map position: 11q12
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin

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  Query Match             23.2%;  Score 398;  DB 2;  Length 380;
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  Matches  100;  Conservative   71;  Mismatches  134;  Indels   38;  Gaps   13;

Qy          1 MEPNGTFSN----NNSRNCTIENFKRE--FFPIVYLIIFFWGVLGNGLSIY-VFLQPYKK 53
              ||  | | |     :|    |    ::|       | :|:::|  |  |||| :: ||     :|
Db          1 MEEGGDFDNYYGADNQSECEYTDWKSSGALIPAIYMLVFLLGTTGNGLVLWTVFRSSREK 60

Qy         54 STSVNVFMLNLAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFL 113
                | ::|: :||::|| |: |||  |  |   |  :| ||    |:: || ::||||:|:: |
Db         61 RRSADIFIASLAVADLTFVVTLPLWATYTYRDYDWPFGTFFCKLSSYLIFVNMYASVFCL 120

Qy        114 TVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWIL--IMASSIML-DSGSEQNGSVTS 170
              | ||  |:||:| |       :      |  :     ::|:|   ::|   :|:|   :|  :| :
Db        121 TGLSFDRYLAIVRPVANARLRLRVSGAVATAVLWVLAALLAMPVMVLRTTGDLENTTKVQ 180

Qy        171 CLELNLYKIAKLQT-------MNYIALVVGCLLPFFTLSICYLLIIRVLL------KVEV 217
              |  ::   :| : :         :   :  || ::||  :  ||   | : :         ::|
Db        181 CY-MDYSMVATVSSEWAWEVGLGVSSTTVGFVVPFTIMLTCYFFIAQTIAGHFRKERIE- 238

Qy        218 PESGLRVSHRKALTTIIITLIIFFLCFLPYHTLRTVH----LTTWKVGLCKDRLHKALVI 273
                 |||    |:  |:  |::  ::  |  ||::|||  ::|::       |     |      |     |       :
Db        239 ---GLR-KRRRLLSIIVVLVVTFALCWMPYHLVKTLYMLGSLLHWP---CDFDLFLMNIF 291

Qy        274 --TLALAAANACFNPLLYYFAGENFKDRLKSALRKGHPQKAKT 314
                    ::   |:|  || |||  |      |:       |   |    |    :  |  |
Db        292 PYCTCISYVNSCLNPFLYAFFDPRFRQACTSMLCCGQSRCAGT 334
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Search completed: October 8, 2003, 08:28:16
Job time : 42 secs